ACCESSION NUMBER: 1999063661 MEDLINE
DOCUMENT NUMBER: 99063661 PubMed ID: 9847150
TITLE: The Mouse Genome **Database** (MGD): genetic and genomic information about the laboratory mouse. The Mouse Genome **Database** Group.
AUTHOR: Blake J A; Richardson J E; Davisson M T; Eppig J T
CORPORATE SOURCE: The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA.. jblake@informatics.jax.org
CONTRACT NUMBER: HG00330 (NHGRI)
SOURCE: NUCLEIC ACIDS RESEARCH, (1999 Jan 1) 27 (1) 95-8. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 20000303
Entered Medline: 19990316

AB The Mouse Genome Database (MGD) focuses on the integration of mapping, homology, polymorphism and molecular data about the laboratory mouse. Detailed descriptions of genes including their chromosomal location, gene function, disease associations, mutant phenotypes, molecular polymorphisms and links to representative sequences including **ESTs** are integrated within MGD. The association of information from experiment to gene to genome requires careful coordination and implementation of standardized vocabularies, unique nomenclature constructions, and detailed information derived from multiple sources. This information is linked to other public databases that focus on additional information such as **expression patterns**, sequences, bibliographic details and large mapping panel data. Scientists participate in the curation of MGD data by generating the Chromosome Committee Reports, consulting on gene family nomenclature revisions, and providing descriptions of mouse strain characteristics and of new mutant phenotypes. MGD is accessible at http://www.informatics.jax.org

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT 19:04:09
ON 08 JUL 2002

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L1         13496 S EST
L2            34 S L1(S)(NO#(W)CORRELAT?)
L3            21 DUP REM L2 (13 DUPLICATES REMOVED)
L4          3375 S L1(S)(MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5          1972 S L4(S)(PROTEIN OR PEPTIDE)
L6          1748 S L5(S)(EXPRESS?)
L7           775 S L6(S)DATABASE#
L8           355 DUP REM L7 (420 DUPLICATES REMOVED)
L9            96 S L8(S)(PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10           47 S L8(S)GENBANK
L11           87 S L8(S)(HEART OR BONE OR BRAIN)
L12          137 S L11 OR L9
L13            1 S L12 AND (NO#(W)EXPRESS?)
L14           67 S L12(S)(TRANSCRI?)
L15           86 S L8(S)NORTHERN
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L16          50 S L1(S)(NO#(2W)CORRELAT?)
L17          16 S L16 NOT L2
L18          12 DUP REM L17 (4 DUPLICATES REMOVED)
L19          54 S L1(S)(NO#(3W)CORRELAT?)
L20           0 S L19 NOT L1
L21          20 S L19 NOT L2
L22           4 S L21 NOT L16

     FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002
L23       13496 S EST OR (SEQUENCE(W)TAG#)
L24         234 S L23 AND DATABASE#/TI
L25           0 S L24 AND (NO(3W)CORRELAT?)
L26         234 S L24(S)DATABASE#
L27        2221 S L23(S)DATABASE#
L28           4 S L27(S)(NO#(3W)CORRELAT?)
L29        1174 S L23(S)(BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30         310 S L29(S)NORTHERN
L31         133 S L30 AND DATABASE#
L32          78 DUP REM L31 (55 DUPLICATES REMOVED)
L33        1072 S L23(S)(PREDICT? OR ANTICIPAT?)
L34          22 S L33 AND DATABASE#/TI
L35          13 DUP REM L34 (9 DUPLICATES REMOVED)
L36          22 S L34(S)DATABASE#
L37        2221 S L23(S)DATABASE#
L38         612 S L37(S)TISSUE
L39          58 S L38(S)PROSTATE
L40          10 S L39 AND PREDICT?
L41           6 DUP REM L40 (4 DUPLICATES REMOVED)
L42           1 S L23(S)(CANNOT(3W)PREDICT)
L43       13596 S L23 OR DBEST
L44        6719 S L43(S)EXPRESS?
L45         192 S L44(S)BLAST
L46          47 S L45(S)PREDICT?
L47          27 DUP REM L46 (20 DUPLICATES REMOVED)
L48           2 S L43(S)RELIED
L49           1 S L43(S)(("NOT" OR CANNOT)(W)PREDICT?)
L50           0 S L43(S)(CANNOT(W)ANTICIPATE)
L51         797 S L43(S)TRANSCRIPTS
L52          28 S L43(S)((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
L53          17 DUP REM L52 (11 DUPLICATES REMOVED)
L54         546 S L43 AND (EXPRESSION(A)PATTERN#)
L55          15 S L54 AND DATABASE#/TI
L56           9 DUP REM L55 (6 DUPLICATES REMOVED)
L57         239 S L43 AND DATABASE#/TI
L58           5 S L57 AND PREDICT
L59           3 DUP REM L58 (2 DUPLICATES REMOVED)
L60        1735 S L43(S)LIBRAR?
L61          34 S L60(S)PREDICT
L62          19 DUP REM L61 (15 DUPLICATES REMOVED)
L63        4276 S L43(S)(MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
L64         335 S L63(S)(EXPRESSION(A)PATTERN#)
L65          86 S L64(S)(PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L66          49 DUP REM L65 (37 DUPLICATES REMOVED)
L67         430 S L43(S)(EXPRESSION(A)PATTERN#)
L68          12 S L67 AND DATABASE#/TI
L69           6 DUP REM L68 (6 DUPLICATES REMOVED)
L70          99 S L23(3A)PREDICT?
L71           2 S L70(3A)(EXPRESSION OR TRANSCRIPTION)
L72         152 S L43(5A)PREDICT?
L73           3 S L72(5A)(EXPRESSION OR TRANSCRIPTION)
L74           1 S L73 NOT L71
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L75          64 S L43(S)HYPOTHETICAL
L76          55 S L75(S)(EXPRESS? OR TRANSCI?)
L77          34 DUP REM L76 (21 DUPLICATES REMOVED)
L78          28 S L30(S)(EXPRESSION(A)PATTERN#)
L79          15 DUP REM L78 (13 DUPLICATES REMOVED)
L80           0 S L23(S)("NOT"(W)PREDICTIVE)
L81           0 S L23(S)(CANNOT(W)ANTICIPATE)
L82         107 S DATABASE(A)MINING
L83          14 S L23 AND L82
L84           8 DUP REM L83 (6 DUPLICATES REMOVED)
L85        2347 S ESTS
L86          79 S L85 AND DATABASE/TI
L87           0 S L86 AND (CANNOT(W)(ANTICIPATE OR PREDICT))
L88           4 S L86 AND (EXPRESSION(A)PATTERN#)
L89           2 DUP REM L88 (2 DUPLICATES REMOVED)

=> s l85 and northern
L90         331 L85 AND NORTHERN

=> s l90 and (expression(a)pattern#)
L91          58 L90 AND (EXPRESSION(A) PATTERN#)

=> dup rem l91
PROCESSING COMPLETED FOR L91
L92          36 DUP REM L91 (22 DUPLICATES REMOVED)

=> d ibib abs tot

L92  ANSWER 1 OF 36     MEDLINE                              DUPLICATE 1
ACCESSION NUMBER:    2002132101     MEDLINE
DOCUMENT NUMBER:     21856794   PubMed ID: 11867260
TITLE:               Digital expression profiles of the prostate
                     androgen-response program.
AUTHOR:              Clegg Nigel; Eroglu Burak; Ferguson Camari; Arnold Hugh;
                     Moorman Alec; Nelson Peter S
CORPORATE SOURCE:    Division of Human Biology, Fred Hutchinson Cancer Research
                     Center, 1100 Fairview Avenue North, Seattle, WA 98109,
USA.
CONTRACT NUMBER:     CA75173 (NCI)
SOURCE:              JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY,
                     (2002 Jan) 80 (1) 13-23.
                     Journal code: 9015483. ISSN: 0960-0760.
PUB. COUNTRY:        England: United Kingdom
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         200205
ENTRY DATE:          Entered STN: 20020228
                     Last Updated on STN: 20020515
                     Entered Medline: 20020514
AB   The androgen receptor (AR) and cognate ligands regulate vital aspects of
     prostate cellular growth and function including proliferation,
     differentiation, apoptosis, lipid metabolism, and secretory action. In
     addition, the AR pathway also influences pathological processes of the
     prostate such as benign prostatic hypertrophy and prostate
carcinogenesis.
     The pivotal role of androgens and the AR in prostate biology prompted
this
     study with the objective of identifying molecular mediators of androgen
     action. Our approach was designed to compare transcriptomes of the LNCaP
     prostate cancer cell line under conditions of androgen depletion and
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androgen stimulation by generating and comparing collections of expressed sequence tags (**ESTs**). A total of 4400 **ESTs** were produced from LNCaP cDNA libraries and these **ESTs** assembled into 2486 distinct transcripts. Rigorous statistical analysis of the expression profiles indicated that 17 genes exhibited a high probability (P>0.9) of androgen-regulated expression. **Northern** analysis confirmed that the expression of KLK3/PSA, FKBP5, KRT18, DKFZP564K247, DDX15, and HSP90 is regulated by androgen exposure. Of these, only KLK3/PSA is known to be androgen-regulated while the other genes represent new members of the androgen-response program in prostate epithelium. LNCaP gene expression profiles defined by two independent experiments using the serial analysis of gene expression (SAGE) method were compared with the EST profiles. Distinctly different **expression patterns** were produced from each dataset. These results are indicative of the sensitivity of the methods to experimental conditions and demonstrate the power and the statistical limitations of digital expression analyses.

L92 ANSWER 2 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:547812 BIOSIS
DOCUMENT NUMBER: PREV200100547812
TITLE: Predicting temporal-spatial gene expression in neuronal progenitors using oligonucleotide microarrays.
AUTHOR(S): Zhao, Q. (1); Kho, A.; Kenney, A. M. (1); Yuk, D. (1); Golub, T. R.; Kohane, I.; Zhang, Y. (1); Rowitch, D. H. (1)
CORPORATE SOURCE: (1) Pediatric Oncology, Dana-Farber Cancer Institute, Boston, MA USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 1525. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The genetic mechanisms regulating proliferation and differentiation of cerebellar granule neuron precursors (CGNP) during development are poorly understood. This issue is of particular interest because CGNP are thought to be the origin of the pediatric brain tumor, medulloblastoma. We have used Affymetrix Mu11K (GeneChips) oligonucleotide microarrays to identify genes upregulated in immature granule cells in primary cultures of post-natal day 5 (PN5) cerebellum when treated with the mitogen, Sonic Hedgehog (SHH). Despite such primary cultures are highly heterogeneous and contain only 15-20% proliferating cells, we observed a rapid upregulation (2-15 folds) of numerous genes when treated with SHH proteins. In contrast, we observed no significant increase in gene expression following growth arrest, suggesting that the granule cells in culture are relatively unresponsive to SHH upon cell cycle exit. Using novel analysis tools, we derived a list of genes/**ESTs** upregulated by Shh treatment and prospectively screened their **expression pattern** by in situ hybridization, RT-PCR and **northern** blot. This method accurately predicted gene expression specifically in the developing external granule cell layer of the PN7 cerebellum in 78% of cases tested. These results demonstrate that appropriate in vitro models in conjunction with oligonucleotide microarrays may be used to accurately predict gene **expression pattern** and gene discovery in proliferating

neural precursors.

L92 ANSWER 3 OF 36 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001228125 MEDLINE
DOCUMENT NUMBER: 21139743 PubMed ID: 11243851
TITLE: Effect of serial passage on gene expression in MC3T3-E1 preosteoblastic cells: a microarray study.
AUTHOR: Huang W; Carlsen B; Rudkin G H; Shah N; Chung C; Ishida K; Yamaguchi D T; Miller T A
CORPORATE SOURCE: Plastic Surgery Section, VA Greater Los Angeles Healthcare System, Los Angeles, California, 90073, USA.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Mar16) 281 (5) 1120-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010502
Last Updated on STN: 20010502
Entered Medline: 20010426

AB The osteoblastic function of mouse preosteoblastic MC3T3-E1 cells, as measured by alkaline phosphatase activity and osteocalcin secretion, decreases after serial passage. To uncover genes responsible for decreased osteoblastic function in high-passage cells, we have studied passage-dependent change of gene expression in MC3T3-E1 cells. Changes in the **expression pattern** of 2000 selected genes were examined simultaneously by comparing mRNA levels between MC3T3-E1 cells at passage 20 and passage 60 using the cDNA microarray analysis. Significant changes in the steady-state abundance of 27 mRNAs were observed in response to different passage numbers, including 17 known genes, 4 **ESTs** with homology to known genes, and 6 genes with no previously described function or homology. **Northern** blot analysis was used to verify and quantify the expression of selected genes, and revealed a significant higher level of up- and down-regulation compared to microarray data. These results indicate the existence of a significant change in gene expression in osteoblastic cells undergoing serial passages. Such changes might be responsible for a reduction in bone regeneration in older osteoblasts. Potential roles of selected genes in bone aging are discussed.

L92 ANSWER 4 OF 36 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001323353 MEDLINE
DOCUMENT NUMBER: 21135671 PubMed ID: 11238394
TITLE: Analysis of expressed sequence tags from two starvation, time-of-day-specific libraries of Neurospora crassa reveals novel clock-controlled genes.
AUTHOR: Zhu H; Nowrousian M; Kupfer D; Colot H V; Berrocal-Tito G; Lai H; Bell-Pedersen D; Roe B A; Loros J J; Dunlap J C
CORPORATE SOURCE: Department of Chemistry and Biochemistry, Advanced Center for Genome Technology, University of Oklahoma, Norman, Oklahoma 73019, USA.
CONTRACT NUMBER: MH44651 (NIMH)
R37-GM 34985 (NIGMS)

SOURCE: GENETICS, (2001 Mar) 157 (3) 1057-65.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF074941; GENBANK-AF277086
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20010611
Entered Medline: 20010607

AB In an effort to determine genes that are expressed in mycelial cultures of Neurospora crassa over the course of the circadian day, we have sequenced 13,000 cDNA clones from two time-of-day-specific libraries (morning and evening library) generating approximately 20,000 sequences. Contig analysis allowed the identification of 445 unique expressed sequence tags (**ESTs**) and 986 **ESTs** present in multiple cDNA clones. For approximately 50% of the sequences (710 of 1431), significant matches to sequences in the National Center for Biotechnology Information database (of known or unknown function) were detected. About 50% of the **ESTs** (721 of 1431) showed no similarity to previously identified genes. We hybridized **Northern** blots with probes derived from 26 clones chosen from contigs identified by multiple cDNA clones and EST sequences. Using these sequences, the representation of genes among the morning and evening sequences, respectively, in most cases does not reflect their **expression patterns** over the course of the day. Nevertheless, we were able to identify four new clock-controlled genes. On the basis of these data we predict that a significant proportion of the expressed Neurospora genes may be regulated by the circadian clock. The mRNA levels of all four genes peak in the subjective morning as is the case with previously identified ccgs.

L92 ANSWER 5 OF 36 MEDLINE
ACCESSION NUMBER: 2001551975 MEDLINE
DOCUMENT NUMBER: 21482651 PubMed ID: 11597177
TITLE: Identification and initial characterization of 5000 expressed sequenced tags (**ESTs**) each from adult human normal and osteoarthritic cartilage cDNA libraries.
AUTHOR: Kumar S; Connor J R; Dodds R A; Halsey W; Van Horn M; Mao J; Sathe G; Mui P; Agarwal P; Badger A M; Lee J C; Gowen M;
Lark M W
CORPORATE SOURCE: Department of Musculoskeletal Diseases, GlaxoSmithKline Pharmaceuticals, 709 Swedeland Rd, King of Prussia, Pennsylvania 19406, USA.. Sanjay_kumar-1@GSK.COM
SOURCE: OSTEOARTHRITIS AND CARTILAGE, (2001 Oct) 9 (7) 641-53.
Journal code: 9305697. ISSN: 1063-4584.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-BG924211; GENBANK-BG924212; GENBANK-BG924213; GENBANK-BG924214; GENBANK-BG924215; GENBANK-BG924216; GENBANK-BG924217; GENBANK-BG924218; GENBANK-BG924219; GENBANK-BG924220; GENBANK-BG924221; GENBANK-BG924222; GENBANK-BG924223; GENBANK-BG924224; GENBANK-BG924225;

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ENTRY MONTH: 200112

ENTRY DATE: Entered STN: 20011015
Last Updated on STN: 20020122
Entered Medline: 20011204

AB OBJECTIVE: To prepare, sequence and analyse adult human cartilage cDNA libraries to study the gene **expression pattern** between normal and osteoarthritic cartilage. METHODS: Poly A(+)RNA from adult human normal and osteoarthritic articular cartilage was isolated and used to prepare cDNA libraries. Approximately 5000 **ESTs** from each library were sequenced and analysed using bioinformatic tools. The expression of select genes was confirmed by **Northern** blot and in situ hybridization analysis. RESULTS: Multiple gene families including several classical cartilage matrix protein encoding genes were identified.

Approximately 28-40% of the genes sequenced from these libraries were novel, while half of the genes encoded known proteins and 4-6% of the genes encoded novel homologs of known proteins. Several known genes, whose expression has not been reported previously in cartilage, were also identified. We have confirmed the cartilage expression of three known (CTGF, CTGF-L and clusterin) and two novel homologs of known genes (PCPE-2 and Gal-Nac transferase) by **Northern** blot and in situ hybridization analysis. CONCLUSION: This is the first report of the preparation and sequencing of cDNA libraries from adult human normal and osteoarthritic articular cartilage. Further analysis of genes identified from these libraries may provide molecular targets for diagnosis and/or treatment of osteoarthritis (OA).

L92 ANSWER 6 OF 36 MEDLINE DUPLICATE 4

ACCESSION NUMBER: 2001553061 MEDLINE

DOCUMENT NUMBER: 21485291 PubMed ID: 11599797

TITLE: Isolation and characterization of a novel cDNA, UBAP1, derived from the tumor suppressor locus in human chromosome 9p21-22.

AUTHOR: Qian J; Yang J; Zhang X; Zhang B; Wang J; Zhou M; Tang K; Li W; Zeng Z; Zhao X; Shen S; Li G
CORPORATE SOURCE: Cancer Research Institute, Human Medical University, Changsha, PR China.
SOURCE: JOURNAL OF CANCER RESEARCH AND CLINICAL ONCOLOGY, (2001 Oct) 127 (10) 613-8.
Journal code: 7902060. ISSN: 0171-5216.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200111
ENTRY DATE: Entered STN: 20011016
Last Updated on STN: 20011105
Entered Medline: 20011101

AB PURPOSE: To clone the putative tumor suppressor gene(s) in a refined region at 9p21-22 undergoing loss of heterozygosity in nasopharyngeal carcinoma (NPC). METHODS: We systematically screened the **expression patterns** of 25 novel **ESTs** (expressed sequence tags) in a minimal common deleted region of 9p21-22 in NPC. One of these **ESTs** was found down-regulated in NPC. Subsequently, the corresponding gene sequence of this EST was established by cDNA cloning and RACE (rapid amplification of cDNA end) procedures. Furthermore, a mouse homologue of this gene was identified. The expression of this gene was examined using **Northern** blot or reverse transcription-polymerase chain reaction (RT-PCR) in various human and mouse tissues. A limited screen for mutation of coding sequence of this novel human gene was undertaken using RT-PCR and direct sequencing analysis. RESULTS: A novel gene was cloned. This gene is a new member of the UBA domain family, so we named it UBAPI for ubiquitin-associated protein 1 (HUGO Gene Nomenclature Committee-approved symbol). **Northern** blot and RT-PCR analysis demonstrate a ubiquitous pattern of gene expression in human and mouse tissues. The direct sequencing analysis of the coding region of hUBAP1 following RT-PCR failed to reveal any mutations in a preliminary screen of NPC cell line HNE1 and primary nasopharyngeal carcinoma samples. CONCLUSIONS: We cloned a novel gene UBAPI, which is highly conserved between human and mouse. Clearly, as a novel member of UBA domain protein family and taking its map location into account, a more extensive analysis is essential to establish whether subtle mutations are present in nasopharyngeal carcinomas.

L92 ANSWER 7 OF 36 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2001413960 MEDLINE
DOCUMENT NUMBER: 21356581 PubMed ID: 11464241
TITLE: Physical and transcriptional map of the hereditary inclusion body myopathy locus on chromosome 9p12-p13.
AUTHOR: Eisenberg I; Hochner H; Shemesh M; Levi T; Potikha T; Sadeh M; Argov Z; Jackson C L; Mitrani-Rosenbaum S
CORPORATE SOURCE: The Unit for Development of Molecular Biology and Genetic Engineering, Hadassah Hospital, The Hebrew University-Hadassah Medical School, Jerusalem 91240, Israel.
SOURCE: EUROPEAN JOURNAL OF HUMAN GENETICS, (2001 Jul) 9 (7) 501-9.
Journal code: 9302235. ISSN: 1018-4813.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20010903
Entered Medline: 20010830

AB Hereditary inclusion body myopathy (HIBM) is a group of neuromuscular disorders characterised by adult-onset, slowly progressive distal and proximal muscle weakness and typical muscle pathology. Previously, we have mapped the gene responsible for a recessive form of HIBM to chromosome 9p1 and narrowed the interval to one single YAC clone of 1 Mb in size. As a further step towards the identification of the HIBM gene, we have constructed a detailed physical and transcriptional map of this region. A high resolution BAC contig that includes the HIBM critical region, flanked by marker 327GT4 and D9S1859, was constructed. This contig allowed the precise localisation of 25 genes and **ESTs** to the proximal region of chromosome 9. The **expression pattern** of those mapped genes and **ESTs** was established by **Northern** blot analysis. In the process of refining the HIBM interval, 13 new polymorphic markers were identified, of which 11 are CA-repeats, and two are single nucleotide polymorphisms. Certainly, this map provides an important integration of physical and transcriptional information corresponding to chromosome 9p12-p13, which is expected to facilitate the cloning and identification not only of the HIBM gene, but also other disease genes which map to this region.

L92 ANSWER 8 OF 36 MEDLINE
ACCESSION NUMBER: 2002057218 MEDLINE
DOCUMENT NUMBER: 21643879 PubMed ID: 11784032
TITLE: Systematic screening and expression analysis of the head organizer genes in Xenopus embryos.
AUTHOR: Shibata M; Itoh M; Ohmori S Y; Shinga J; Taira M
CORPORATE SOURCE: Department of Biological Sciences, Graduate School of Science, University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan.
SOURCE: DEVELOPMENTAL BIOLOGY, (2001 Nov 15) 239 (2) 241-56. Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020131
Entered Medline: 20020130

AB We describe here a systematic screen of an anterior endomesoderm (AEM) cDNA library to isolate novel genes which are expressed in the head organizer region. After removing clones which hybridized to labeled cDNA probes synthesized with total RNA from a trunk region of tailbud embryos, the 5' ends of 1039 randomly picked cDNA clones were sequenced to make expressed sequence tags (**ESTs**), which formed 754 tentative unique clusters. Those clusters were compared against public databases and classified according to similarities found to other genes and gene products. Of them, 151 clusters were identified as known Xenopus genes, including eight organizer-specific ones (5.3%). Gene **expression**

pattern screening was performed for 198 unique clones, which were selected because they either have no known function or are predicted to be developmental regulators in other species. The screen revealed nine possible organizer-specific clones (4.5%), four of which appeared to be expressed in the head organizer region. Detailed expression analysis from gastrula to neurula stages showed that these four genes named crescent, P7E4 (homologous to human hypothetical genes), P8F7 (an unclassified gene), and P17F11 (homologous to human and Arabidopsis hypothetical genes) demarcate spatiotemporally distinct subregions of the AEM corresponding to the head organizer region. These results indicate that our screening strategy is effective in isolating novel region-specific genes.

L92 ANSWER 9 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:138979 BIOSIS
DOCUMENT NUMBER: PREV200200138979
TITLE: Analysis of gene expression during flowering in apomeiotic mutants of Medicago spp.: Cloning of **ESTs** and candidate genes for 2n eggs.
AUTHOR(S): Barcaccia, Gianni (1); Varotto, Serena; Meneghetti, Stefano; Albertini, Emidio; Porceddu, Andrea; Parrini, Paolo; Lucchin, Margherita
CORPORATE SOURCE: (1) Dipartimento di Agronomia Ambientale e Produzioni Vegetali, University of Padua, Agripolis, Via Romea 16, 35020, Legnaro, Padua: gianni.barcaccia@unipd.it Italy
SOURCE: Sexual Plant Reproduction, (December, 2001) Vol. 14, No. 4, pp. 233-238. print.
ISSN: 0934-0882.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Mutants showing features of apomixis have been documented in alfalfa (Medicago sativa L.), a natural outcrossing sexual species. A differential display of mRNAs that combines cDNA-AFLP markers and bulked segregant analysis was carried out with the aim of selecting expressed sequence tags (**ESTs**) and cloning candidate genes for apomeiosis in mutants of alfalfa characterized by 2n egg formation at high frequencies. The approach enabled us to select either mutant- or wild type-specific transcript derived-fragments and to detect transcriptional changes potentially related to 2n eggs. Sequence alignments of a subset of 40 polymorphic clones showed significant homologies to genes of known function. An EST with identity to a beta-tubulin gene, highly expressed in the wild type and poorly expressed in the apomeiotic mutants, and an EST with identity to a Mob1-like gene, qualitatively polymorphic between pre- and post-meiotic stages, were selected as candidate genes for apomeiosis because of their putative roles in the cell cycle. A number of clone-specific primers were designed for performing both 5' and 3' rapid amplification of cDNA ends to obtain the full-length clones. Southern blot hybridization revealed that both clones belong to a multi-gene family with a minimum of three genomic DNA members each. **Northern** blot hybridization of total RNA samples and in situ hybridization of whole buds enabled the definition of their temporal and spatial **expression**

patterns in reproductive organs. Experimental achievements towards the elucidation of apomeiotic megasporogenesis in alfalfa are presented and discussed.

L92 ANSWER 10 OF 36 MEDLINE
ACCESSION NUMBER: 2001314104 MEDLINE
DOCUMENT NUMBER: 21280915 PubMed ID: 11386757
TITLE: Central nervous system, uterus, heart, and leukocyte expression of the LOXL3 gene, encoding a novel lysyl oxidase-like protein.
AUTHOR: Jourdan-Le Saux C; Tomsche A; Ujfalusi A; Jia L; Csiszar K
CORPORATE SOURCE: Pacific Biomedical Research Center, University of Hawaii, 1993 East-West Road, Honolulu, Hawaii, 96822.
CONTRACT NUMBER: CA76580 (NCI)
RR03061 (NCRR)
SOURCE: GENOMICS, (2001 Jun 1) 74 (2) 211-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA852888; GENBANK-AF311313; GENBANK-AI752772; GENBANK-R55706
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20011008
Last Updated on STN: 20011008
Entered Medline: 20011004

AB A BLASTN search using the mouse lor-2 cDNA identified three overlapping **ESTs** (AI752772, AA852888, and R55706) in the GenBank database. These expressed sequence tags were assembled into a contig of 3121 nucleotides with an open reading frame of 2262 bp. The encoded putative polypeptide of 754 amino acids presented all structural characteristics of the lysyl oxidase (LOX) enzyme family, a copper-binding site with four histidyl residues, the lysyl and tyrosyl residues known to be involved in LOX enzyme in the formation of the quinone cofactor and surrounding sequences, and the cytokine receptor-like domain. In addition, four scavenger receptor cysteine-rich (SRCR) domains were found in the N-terminal region of the protein. The gene encoding this new cDNA, which we have referred to as human lysyl oxidase-like 3 (humanLOXL3), has been mapped to chromosome 2p13.3, overlapping at its 3' end the HtrA2 serine protease gene. The structure of the humanLOXL3 gene was deduced from the BAC clone bac91a19 sequence and contained 14 exons. The **expression pattern** of this new member of the LOX gene family appears to be different from that of the LOX and LOX-like genes, as the central nervous system, neurons, and also leukocytes expressed humanLOXL3. A BLASTN search of the human EST database indicated the presence of **ESTs**, corresponding to alternative splice variants of LOXL3, that lacked exon 5 and exon 8. The putative resulting protein retained the region encoding the structural and functional elements of the amine oxidase but the second and fourth SRCR domains were truncated and the potential BMP-1 cleavage site was not present. The presence of domains unrelated to the traditional amine oxidase activity is a strong indication that humanLOXL3 might fulfill other functions in addition to intrinsic enzyme activity.

L92 ANSWER 11 OF 36 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2002184690 MEDLINE

DOCUMENT NUMBER: 21914855 PubMed ID: 11917942
TITLE: Identification of a gene frequently mutated in prostate tumors.
AUTHOR: Reding D J; Zhang K Q; Salzman S A; Thomalla J V; Riepe R E; Suarez B K; Catalona W J; Burmester J K
CORPORATE SOURCE: Department of Hematology, Marshfield Clinic, WI, USA.
CONTRACT NUMBER: MH31302 (NIMH)
SOURCE: MEDICAL ONCOLOGY, (2001) 18 (3) 179-87.
Journal code: 9435512. ISSN: 1357-0560.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020424
Entered Medline: 20020423

AB Although prostate cancer is the second leading cause of cancer death for men in the United States, the genetics of tumor development are poorly understood. Several expressed sequence tagged genes (**ESTs**) that are expressed predominantly in the prostate have recently been identified, although their role in the development and maintenance of the prostate is unknown. Here, we demonstrate that the gene identified as UNIGENE cluster Hs. 104215, which codes for a message found predominantly in the prostate, may be important in tumor development. We name this gene PCan1 for Prostate Cancer gene 1. **Northern** blot experiments were performed using RNA isolated from tumor-derived cell lines and human prostate to determine the **expression pattern** of the gene. DNA sequencing was used to identify mutations that occurred in tumor tissue. By **Northern** blot analysis, this gene product was not detectable in LNCaP, DU 145, or PC-3 prostate cancer cell lines, although it was readily observed in RNA isolated from total prostate and from dissected central and peripheral regions of prostate. Sequence analysis of genomic DNA from LNCaP, DU 145, or PC-3 cells demonstrated a G/A polymorphism at position 193. Analysis of matched tumor-derived DNA and blood-derived DNA samples from 11 of 13 patients who had undergone a radical prostatectomy and who were homozygous for A in blood-derived DNA demonstrated mutation of position 193 in matched tumor samples resulting in G/A polymorphism. Sixteen additional patient samples were G/A polymorphic in both blood-derived DNA and tumor-derived DNA and two samples were GG in both blood-derived and tumor-derived DNA. Our results suggest that this gene may be a hot spot for mutation in prostate cancer, especially because our radiation hybrid mapping located this gene within a region identified in linkage mapping studies of affected families with prostate cancer. Loss of heterozygosity in prostate tumors has also been reported at the location of PCan1. Further studies to determine the functional role of this candidate tumor suppressor gene are warranted.

L92 ANSWER 12 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:270176 BIOSIS
DOCUMENT NUMBER: PREV200100270176
TITLE: Cloning and expression analysis of a novel gene, UBAP1, possibly involved in ubiquitin pathway.
AUTHOR(S): Qian Jun; Zhang Xiao-Hui; Yang Jian-Bo; Wang Jie-Ru; Zhang Bi-Cheng; Tang Ke; Li Gui-Yuan (1)
CORPORATE SOURCE: (1) Cancer Research Institute, Hunan Medical University, Changsha, 410078: ligy@cs.hn.cn China
SOURCE: Shengwu Huaxue yu Shengwu Wuli Xuebao, (2001) Vol. 33, No.

2, pp. 147-152. print.
ISSN: 0582-9879.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: Chinese; English
AB The 9p21-22 region shows loss of heterozygosity in up to 60% of human nasopharyngeal carcinomas (NPC), indicating the presence of a tumor suppressor gene in this region. We have identified a novel minimal common deletion region at 9p21-22. Twenty-two epithelial-derived expressed sequence tags(**ESTs**) in this critical region were systematically screened by differential RT-PCR to investigate the **expression patterns** in NPC cell line HNE1 and primary cultures of normal nasopharyngeal epithelial cells. One of these **ESTs** was found down-expressed in HNE1, whose differential expression was confirmed by **Northern** blot. Subsequently the corresponding gene sequence for this EST was established by cDNA cloning and RACE procedures (GenBank Accession No. AF222043). Furthermore, a mouse homologue of this gene was identified (GenBank Accession No. AF275549). This gene is 2.7 kb long and contains two UBA domains. It is a new member of UBA domain protein family, encoding a putative protein of 502 amino acids with a theoretical molecular mass of 55 kD, so we have named this gene UBAP1 for ubiquitin associated protein 1 (HUGO Gene Nomenclature Committee-approved symbol). **Northern** blot and RT-PCR analysis demonstrated a ubiquitous pattern of gene expression in human and mouse tissues. Direct sequencing analysis of the coding region of hUBAP1 following RT-PCR failed to reveal any mutations in a preliminary screening of NPC cell line HNE1 and primary nasopharyngeal carcinomas samples. However, more detailed analysis is to be performed to reveal if fine mutations of this gene are present in NPC.

L92 ANSWER 13 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151838 BIOSIS
DOCUMENT NUMBER: PREV200200151838
TITLE: Gene **expression patterns** in primary and cultured bone marrow cells.
AUTHOR(S): Ma, Xianyong (1); Degar, Barbara; Wang, Lin (1); Krause, Diane S. (1); Perkins, Archibald S.
CORPORATE SOURCE: (1) Dept. of Laboratory Medicine, Yale University School of Medicine, New Haven, CT USA
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 118b. http://www.bloodjournal.org/. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB With the goal of creating a resource for in-depth study of myelopoiesis, we have executed a two-pronged strategy to obtain a cDNA clone set enriched in myeloid genes. First, we enriched two hematopoietic cDNA libraries for low copy genes. Libraries were prepared from EML cells and their differentiated counterparts, and from Lin-Hoechstlow Rhodaminelow primary murine bone marrow cells. The subtractions were performed using 10,000 known genes and **ESTs** as driver, the ssDNA were purified by hydroxyl appetite chromatography column and used to construct the subtracted cDNA library. 3228 randomly picked clones from the subtracted cDNA libraries represent 1456 distinct genes, of which 649 (45%) are known

named genes, 417 (29%) match uncharacterized **ESTs**, and 345 (24%) are novel sequences. The second aspect of our strategy was to complement this subtracted library with genes known to be involved in myeloid cell differentiation and function. The resulting cDNAs were arrayed on polylysine-coated glass slides. Microarrays were used to analyze changes in gene **expression patterns** during myeloid differentiation. Mouse primary bone marrow cells were fractionated into Lin+, Lin-, (Lin- Hoechest low/Rhodamine Bright), and (Lin- Hoechst low/Rhodamine low) sub-populations. cDNA was prepared from these populations, labeled with Cy3-dCTP or Cy5-dCTP fluorescent nucleotides by PCR amplification, and then hybridized to microarray slides to assess gene expression paterns. Cluster and tree view programs were used to arrange the gene **expression pattern**. **Northern** blot or pseudo-**Northern** blot was used to confirm the microarray data. Analysis indicated that there were abundant changes in gene expression during differentiation. 226 novel genes and 1320 known genes (e.g. DKFZ, SOX4, Ftp-3, Her, Tpd52, Wnt1, FWD2) were down regulated, and 88 novel genes and 1052 known genes (e.g. Agx-1, Mint, Granzyme A, PEBP2aB2, LKLF, ATRN) were up regulated. We focused on several novel genes that we identified as being downregulated very early in hematopoiesis. One of them was cloned and identified as a new member of receptor activity modifying proteins (RAMPs) family called RAMP4, which is highly homologous to RAMP2. However, the transcript is significant larger (apprx7.5kb). When EML (myeloid stem cell line) cells are induced to differentiate with all-trans retinoic acid and IL3, RAMP4 expression levels decrease dramatically within 6 hrs and expression levels remains low thereafter. Consistent with this, Epro (myeloid progenitor cell line) cells express RAMP4 at very low levels. RAMP family members assist in intracellular trafficking of calcitonin receptor and G protein-coupled receptor proteins to the cell surface and thus help dictate the expression of unique cellular phenotypes. Therefore these results suggest the new RAMP may play an important role in myeloid stem cell differentiation and blood cell development. The study for complete physical map and biological function of RAMP-4 are progressing.

L92 ANSWER 14 OF 36 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001676977 MEDLINE
DOCUMENT NUMBER: 21579789 PubMed ID: 11722847
TITLE: Genomic organization and expression profile of the parvin family of focal adhesion proteins in mice and humans.
AUTHOR: Korenbaum E; Olski T M; Noegel A A
CORPORATE SOURCE: Institute for Biochemistry I, Medical Faculty, University of Cologne, Joseph-Stelzmann-Strasse 52, 50931, Cologne, Germany.. elena.korenbaum@uni-koeln.de
SOURCE: GENE, (2001 Nov 14) 279 (1) 69-79.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011128
Last Updated on STN: 20020125
Entered Medline: 20020116

AB We have characterized the genomic organization and the **expression pattern** of alpha-, beta- and gamma-parvin, a novel family of focal

adhesion proteins, in mice and humans. alpha-Parvin is nearly ubiquitously expressed, beta-parvin is preferentially expressed in heart- and skeletal muscle, and gamma-parvin in lymphoid tissues. Parvins display diverse patterns of developmental regulation. The alpha-form is present throughout mouse development, beta-parvin is gradually upregulated and gamma-parvin is downregulated at embryonic day 11. The human alpha-parvin gene (PARVA), extending over 160 kb, is located on chromosome 11. Both, the human beta-parvin gene (PARVB), which is over 145 kb long, and the gamma-parvin gene (PARVG) of a total length of about 25 kb are positioned on chromosome 22 with PARVG located about 12 kb downstream of the 3' end of PARVB. Multiple tissue array analysis indicates that parvins are expressed at reduced levels in cancer as compared to the corresponding normal tissues. Analysis of **ESTs** and PCR-amplified fragments reveals alternatively spliced and alternatively polyadenylated gene products. Mammalian parvins are likely to have arisen late in evolution from gene duplication as they share a remarkably similar exon/intron organization, which is different from the organization of the single genes encoding parvin-like proteins in Drosophila and Caenorhabditis.

L92 ANSWER 15 OF 36 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2002047669 MEDLINE
DOCUMENT NUMBER: 21632271 PubMed ID: 11775832
TITLE: Biological function of a novel gene overexpressed in human hepatocellular carcinoma.
AUTHOR: Liu J; Zhou R; Zhang N; Rui J; Jin C
CORPORATE SOURCE: Department of Cell Biology, Beijing Medical University, Beijing 100083, China.
SOURCE: CHINESE MEDICAL JOURNAL, (2000 Oct) 113 (10) 881-5. Journal code: 7513795. ISSN: 0366-6999.
PUB. COUNTRY: China
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020215
Entered Medline: 20020214

AB OBJECTIVE: To clone the full-length of a differentially expressed cDNA fragment, LC27, and study its biological function tentatively. METHODS: **Northern** blot was used to analyze the **expression pattern** of LC27 in hepatocellular carcinoma, matched nontumor liver tissues, fetal liver and normal adult liver tissues, as well as BEL-7402 hepatocellular carcinoma cell line **ESTs** splicing and 5' rapid amplification of cDNA ends (5' RACE) were used to clone the full-length of LC27 cDNA. An antisense oligodeoxynucleotide approach was used to investigate the biological role of the gene in the proliferation of BEL-7402 cells. RESULTS: A 2186 bp novel cDNA with an open reading frame encoding a 283 amino acid protein was cloned. Analysis of the deduced amino acid sequence indicated that it is 38% (88/229) identical to human Golgi 4-transmembrane spanning transporter MTP. The gene and the encoded protein was termed hepatocellular carcinoma overexpressed transmembrane protein (hotp) and HOTP, respectively. Hotp mRNA was almost undetectable in normal adult liver and fetal liver tissues. However, it was significantly up-regulated in hepatocellular carcinoma and some matched nontumor liver tissues, as well as BEL-7402 cells. The proliferation of BEL-7402 cells was suppressed by an antisense

oligodeoxynucleotide against hotp mRNA at a concentration of 50 micrograms/ml. CONCLUSION: HOTP may be an integral membrane transporter protein. The overexpression of the gene in hepatocellular carcinoma may play an important role in hepatocarcinogenesis and disease progression.

L92 ANSWER 16 OF 36 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2000412547 MEDLINE
DOCUMENT NUMBER: 20366141 PubMed ID: 10903849
TITLE: A 1.5-Mb physical map of the hidrotic ectodermal dysplasia (Clouston syndrome) gene region on human chromosome 13q11.
AUTHOR: Lamartine J; Pitaval A; Soularue P; Lanneluc I; Lemaitre G;
Kibar Z; Rouleau G A; Waksman G
CORPORATE SOURCE: Laboratoire "Genetique des Maladies Dermatologiques,", Universite Evry-Val d'Essonne, Evry, France.
SOURCE: GENOMICS, (2000 Jul 15) 67 (2) 232-6.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000829

AB The HED (hidrotic ectodermal dysplasia) or Clouston syndrome gene (named ED2) has been mapped to the pericentromeric region of chromosome 13 (13q11) to a 2.4-cM interval flanked by markers D13S1828 and D13S1830. We have developed a BAC/PAC-based contig map of this region. This contig, comprising 23 clones and spanning 1.5 Mb, was established by mapping of 27 BAC/PAC end-derived STSs, 11 known polymorphic markers, 2 previously mapped genes, and 14 **ESTs**. The genomic clone overlaps were confirmed by restriction fragment fingerprint analysis. This contig provides the basis for genomic sequencing and gene identification in the ED2 critical region. Of the 14 **ESTs** mapped to the contig, 6 show homology to human genes and 8 appear to be novel. **Expression patterns** of the genes/**ESTs** were tested by **Northern** blot and RT-PCR. Full characterization of some of these genes, as well as the novel **ESTs**, will be useful in assessing their involvement in the HED/Clouston syndrome.

L92 ANSWER 17 OF 36 MEDLINE
ACCESSION NUMBER: 2001089685 MEDLINE
DOCUMENT NUMBER: 20422673 PubMed ID: 10964518
TITLE: Identification of differentially expressed genes in epithelial stem/progenitor cells of fetal rat liver.
AUTHOR: Petkov P M; Kim K; Sandhu J; Shafritz D A; Dabeva M D
CORPORATE SOURCE: The Marion Bessin Liver Research Center, Albert Einstein College of Medicine, Bronx, New York 10461, USA.
CONTRACT NUMBER: P30 DK41296 (NIDDK)
R37 DK17609 (NIDDK)
RO1 DK50636 (NIDDK)
SOURCE: GENOMICS, (2000 Sep 1) 68 (2) 197-209.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AW697795; GENBANK-AW697796; GENBANK-AW697797; GENBANK-AW697798; GENBANK-AW697799; GENBANK-AW697800; GENBANK-AW697801; GENBANK-AW697803; GENBANK-AW697804; GENBANK-AW697805; GENBANK-AW697806; GENBANK-AW697807; GENBANK-AW697808; GENBANK-AW697809; GENBANK-AW697810; GENBANK-AW697811; GENBANK-AW697812; GENBANK-AW697813; GENBANK-AW697814; GENBANK-AW697815; GENBANK-AW697816; GENBANK-AW697817
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010125

AB Differentially expressed cDNA clones from fetal rat liver were isolated using suppression subtractive hybridization, combined with an efficient screening strategy. Approximately 30,000 clones were screened, yielding 643 genes whose expression was induced, of which 201 clones were distinct and 68 represented **ESTs** or newly discovered genes of unknown function. Based on their **expression patterns** in different organs, fetal liver, liver regeneration models, and gut epithelial progenitor cell lines, the subtracted clones presented in this work were placed into four categories: (1) hepatoblast-specific genes; (2) hematopoietic cell-specific genes; (3) genes expressed in hepatoblasts, in hematopoietic cells, and at varying levels in other tissues; and (4) genes overexpressed in fetal liver, in models of activation of liver progenitor cells, and in epithelial progenitor cell lines. Hepatoblast-specific clones and those representing genes induced during liver regeneration are under further study to define their specific function(s) in liver cell growth control and/or differentiation.

L92 ANSWER 18 OF 36 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2000120379 MEDLINE
DOCUMENT NUMBER: 20120379 PubMed ID: 10656586
TITLE: Analysis of Medicago truncatula nodule expressed sequence tags.
AUTHOR: Gyorgyey J; Vaubert D; Jimenez-Zurdo J I; Charon C; Troussard L; Kondorosi A; Kondorosi E
CORPORATE SOURCE: Institut des Sciences Vegetales, CNRS, Gif-sur-Yvette, France.
SOURCE: MOLECULAR PLANT-MICROBE INTERACTIONS, (2000 Jan) 13 (1) 62-71.
Journal code: 9107902. ISSN: 0894-0282.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ388667; GENBANK-AJ388668; GENBANK-AJ388669; GENBANK-AJ388670; GENBANK-AJ388671; GENBANK-AJ388672; GENBANK-AJ388673; GENBANK-AJ388674; GENBANK-AJ388675; GENBANK-AJ388676; GENBANK-AJ388677; GENBANK-AJ388678; GENBANK-AJ388679; GENBANK-AJ388680; GENBANK-AJ388681; GENBANK-AJ388682; GENBANK-AJ388683; GENBANK-AJ388684; GENBANK-AJ388685; GENBANK-AJ388686; GENBANK-AJ388687; GENBANK-AJ388688; GENBANK-AJ388689; GENBANK-AJ388690; GENBANK-AJ388691; GENBANK-AJ388692; GENBANK-AJ388693; GENBANK-AJ388694; GENBANK-AJ388695; GENBANK-AJ388696; +
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000314

Last Updated on STN: 20000314
Entered Medline: 20000229

AB Systematic sequencing of expressed sequence tags (**ESTs**) can give a global picture of the assembly of genes involved in the development and function of organs. Indeterminate nodules representing different stages of the developmental program are especially suited to the study of organogenesis. With the vector lambdaHybriZAP, a cDNA library was constructed from emerging nodules of Medicago truncatula induced by Sinorhizobium meliloti. The 5' ends of 389 cDNA clones were sequenced, then these **ESTs** were analyzed both by sequence homology search and by studying their expression in roots and nodules. Two hundred fifty-six **ESTs** exhibited significant similarities to characterized data base entries and 40 of them represented 26 nodulin genes, while 133 had no similarity to sequences with known function. Only 60 out of the 389 cDNA clones corresponded to previously submitted M. truncatula EST sequences. For 117 cDNAs, reverse **Northern** (RNA) hybridization with root and nodule RNA probes revealed enhanced expression in the nodule, 48 clones are likely to code for novel nodulins, 33 cDNAs are clones of already known nodulin genes, and 36 clones exhibit similarity to other characterized genes. Thus, systematic analysis of the EST sequences and their **expression patterns** is a powerful way to identify nodule-specific and nodulation-related genes.

L92 ANSWER 19 OF 36 MEDLINE

ACCESSION NUMBER: 2000304749 MEDLINE
DOCUMENT NUMBER: 20304749 PubMed ID: 10843801
TITLE: Transcription mapping of the 5q- syndrome critical region: cloning of two novel genes and sequencing, expression, and mapping of a further six novel cDNAs.
AUTHOR: Boultwood J; Fidler C; Strickson A J; Watkins F; Kostrzewa M; Jaju R J; Muller U; Wainscoat J S
CORPORATE SOURCE: Leukaemia Research Fund Molecular Haematology Unit, John Radcliffe Hospital, Headington, 0X3 9DU, United Kingdom.. jboultwo@enterprise.molbiol
SOURCE: GENOMICS, (2000 May 15) 66 (1) 26-34.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF156165; GENBANK-AF157115; GENBANK-AF157116; GENBANK-AF159165; GENBANK-AF159700
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

AB The 5q- syndrome is a myelodysplastic syndrome with the 5q deletion del(5q) as the sole karyotypic abnormality. We are using the expressed sequence tag (EST) resource as our primary approach to identifying novel candidate genes for the 5q- syndrome. Seventeen **ESTs** were identified from the Human Gene Map at the National Center for Biotechnology Information that had no significant homology to any known genes and were assigned between DNA markers D5S413 and D5S487, flanking the critical region of the 5q- syndrome at 5q31-q32. Eleven of the 17 cDNAs from which the **ESTs** were derived (65%) were shown to map to the critical region of the 5q- syndrome by gene dosage analysis and were then sublocalized by PCR screening to a YAC contig encompassing the critical region. Eight of the 11 cDNA clones, upon full sequencing, had no

significant homology to any known genes. Each of the 8 cDNA clones was shown to be expressed in human bone marrow. The complete coding sequence was obtained for 2 of the novel genes, termed C5orf3 and C5orf4. The 2.6-kb transcript of C5orf3 encodes a putative 505-amino-acid protein and contains an ATP/GTP-binding site motif A (P loop), suggesting that this novel gene encodes an ATP- or a GTP-binding protein. The novel gene C5orf4 has a transcript of 3.1 kb, encoding a putative 144-amino-acid protein. We describe the cloning of 2 novel human genes and the sequencing, **expression patterns**, and mapping to the critical region of the 5q- syndrome of a further 6 novel cDNA clones. Genomic localization and **expression patterns** would suggest that the 8 novel cDNAs described in this report represent potential candidate genes for the 5q- syndrome.

L92 ANSWER 20 OF 36 MEDLINE DUPLICATE 11

ACCESSION NUMBER: 2000057833 MEDLINE
DOCUMENT NUMBER: 20057833 PubMed ID: 10588946
TITLE: Family of human oxysterol binding protein (OSBP) homologues. A novel member implicated in brain sterol metabolism.
AUTHOR: Laitinen S; Olkkonen V M; Ehnholm C; Ikonen E
CORPORATE SOURCE: Department of Biochemistry, National Public Health Institute, Mannerheimintie 166, 00300, Helsinki, Finland.
SOURCE: JOURNAL OF LIPID RESEARCH, (1999 Dec) 40 (12) 2204-11. Journal code: 0376606. ISSN: 0022-2275.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000218
Last Updated on STN: 20000218
Entered Medline: 20000210

AB Oxysterol binding protein (OSBP) is a cytosolic protein that undergoes ligand-induced binding to the Golgi apparatus and has been implicated in the regulation of cellular cholesterol metabolism. In the yeast Saccharomyces cerevisiae an OSBP homologue is involved in membrane trafficking through the Golgi complex. Prompted by the multitude of OSBP-related genes in the yeast genome, we carried out a search for human expressed sequence tags (**ESTs**) displaying homology to the sterol-binding domain of OSBP. This revealed a minimum of six novel OSBP-related proteins, designated ORP-1 to ORP-6. ORP cDNA probes were generated by reverse transcription-PCR from human liver mRNA, and used for **Northern** blot analysis of human tissue transcript panels. This verified that each of them represents a different gene product and showed that they display distinct tissue-specific **expression patterns**. The ORP-1 and -2 mRNA expression levels were similar to or higher than that of OSBP while the ORP-3 to -6 mRNAs were detected at lower levels in specific tissues. The most abundantly expressed new gene, ORP-1, was transcribed at strikingly high levels in the cortical areas of human brain and displayed sterol-regulated expression in a cultured human neuroblastoma cell line. This indicates that ORP-1 may play an important role in maintaining the sterol balance in cells of the central nervous system. Together with OSBP, the identified gene products constitute a novel human protein family that may provide a link between organellar

sterol status and membrane dynamics.

L92 ANSWER 21 OF 36 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 1999400797 MEDLINE
DOCUMENT NUMBER: 99400797 PubMed ID: 10471358
TITLE: Chromosomal, in silico and in vitro expression analysis of cardiovascular-based genes encoding zinc finger proteins.
AUTHOR: Dai K S; Liew C C
CORPORATE SOURCE: The Cardiac Gene Unit, Institute of Medical Science Department of Laboratory Medicine and Pathobiology, University of Toronto, Ontario, Canada.
SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1999 Sep) 31
(9) 1749-69.
Journal code: 0262322. ISSN: 0022-2828.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991014
Last Updated on STN: 19991014
Entered Medline: 19991004

AB Three hundred and sixty expressed sequence tags (**ESTs**) from human heart cDNA libraries corresponding to one hundred and twenty six unique zinc finger proteins (ZFPs) were annotated and classified into seven types of ZFPs as reported previously. Among these 126 cvbZFPs (cardiovascular-based ZFPs), the C(2)H(2)-type and the C(2)C(2)-type are the two major ZFP types which account for more than 80% of ZFP genes present in the cardiovascular system. The **expression patterns** of 11 randomly selected ZFP genes (at least one for each type) in normal fetal, adult and hypertrophic adult hearts, respectively, were determined using reverse transcriptase-polymerase chain reaction (RT-PCR) analysis. The results suggest that ZFPs may be involved in the processes of either developmental control (downregulated or upregulated expression) or basic cellular functional regulation (constant expression).

Interestingly, PAF-1 (peroxisome assembly factor-1), a C(3)HC(4)-type ZFP (RING domain-containing ZFP) showing a downregulated **expression pattern** in normal tissues was found to be upregulated in hypertrophic adult heart, suggesting a possible role for this fetal gene in the pathogenesis of cardiac hypertrophy. In silico **Northern** analysis of 15 tissues showed that over 90% of cvbZFPs demonstrate widespread tissue distribution, suggesting the vast majority of ZFPs are functionally shared among tissues. The potential importance of transcriptional repressors in cardiovascular development and disease, such as HFHZ, was supported by the observation that one-third (39 of 126) of cvbZFPs possess this function. Of these, 26 are C(2)H(2)-type and the remaining 13 included 8 C(2)C(2)-type, 1 C(3)HC(4)-type, 1 C(2)HC(4)C(HD)-type, 2 C(3)H-type and 1 combination type. Of particular interest was the observation that ZFPs which contain a KRAB domain are the major subtype present (51. 3% of the total repressors in cvbZFPs). Chromosomal distribution analysis showed that mapping loci of cvbZFP genes are concentrated on chromosomes 1, 3, 6, 8, 10, 11, 12, 19 and X. In particular, chromosome 19 appears to be enriched in ZFP genes with C(2)H(2)-type as the predominant type present. Overall, this report provides a fundamental initial step toward understanding the potential role of ZFPs in regulating cadiac development and disease.

L92 ANSWER 22 OF 36 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 1999210390 MEDLINE
DOCUMENT NUMBER: 99210390 PubMed ID: 10192770
TITLE: Application of a rapid method (targeted display) for the identification of differentially expressed mRNAs following NGF-induced neuronal differentiation in PC12 cells.
AUTHOR: Brown A J; Hutchings C; Burke J F; Mayne L V
CORPORATE SOURCE: Department of Biochemistry, University of Sussex, Falmer, Brighton, BN1 9RY, United Kingdom.
SOURCE: MOLECULAR AND CELLULAR NEUROSCIENCES, (1999 Feb) 13 (2) 119-30.
Journal code: 9100095. ISSN: 1044-7431.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990618
Last Updated on STN: 20020420
Entered Medline: 19990610

AB Nerve growth factor (NGF)-induced differentiation of the rat pheochromocytoma, PC12, cell line presents a model system for the study of early gene expression changes involved in neuronal differentiation. Rapid alterations in mRNA **expression patterns** were investigated in PC12 cells following exposure to NGF using a set of statistically designed primers that exhibit coding-strand bias, and the products were analyzed on agarose gels. This simple and rapid method (targeted display) generated reproducible expression profiles, indicating a complex pattern of gene regulation, and resulted in the identification of a number of NGF-regulated transcripts. Thirty-two of these were selected at random and sequenced, revealing 19 known and 13 novel genes (or **ESTs**). **Northern** blot analysis and RT-PCR confirmed the differential regulation of 22 genes (16 known, 6 novel) and demonstrated 1 false positive result. Antisense application of one isolated gene product, the serine/threonine kinase MARK1, prevented neuronal differentiation in transiently transfected PC12 cells.

L92 ANSWER 23 OF 36 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 1998250717 MEDLINE
DOCUMENT NUMBER: 98250717 PubMed ID: 9582303
TITLE: A family of human beta3-galactosyltransferases. Characterization of four members of a UDP-galactose:beta-N-acetyl-glucosamine/beta-nacetyl-galactosamine beta-1,3-galactosyltransferase family.
AUTHOR: Amado M; Almeida R; Carneiro F; Levery S B; Holmes E H; Nomoto M; Hollingsworth M A; Hassan H; Schwientek T; Nielsen P A; Bennett E P; Clausen H
CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle 20, 2200 Copenhagen N, Denmark.
CONTRACT NUMBER: 1 RO1 CA66234 (NCI)
RO1 CA41521 (NCI)
RO1 CA70740 (NCI)
+
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 May 22) 273 (21) 12770-8.
Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y15060; GENBANK-Y15061; GENBANK-Y15062
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 19980708
Entered Medline: 19980625

AB BLAST analysis of expressed sequence tags (**ESTs**) using the coding sequence of a human UDP-galactose:beta-N-acetyl-glucosamine beta-1, 3-galactosyltransferase, designated beta3Gal-T1, revealed no **ESTs** with identical sequences but a large number with similarity. Three different sets of overlapping **ESTs** with sequence similarities to beta3Gal-T1 were compiled, and complete coding regions of these genes were obtained. Expression of two of these genes in the Baculo virus system showed that one represented a UDP-galactose:beta-N-acetyl-glucosamine beta-1, 3-galactosyltransferase (beta3Gal-T2) with similar kinetic properties as beta3Gal-T1. Another gene represented a UDP-galactose:beta-N-acetyl-galactosamine beta-1, 3-galactosyltransferase (beta3Gal-T4) involved in GM1/GD1 ganglioside synthesis, and this gene was highly similar to a recently reported rat GD1 synthase (Miyazaki, H., Fukumoto, S., Okada, M., Hasegawa, T., and Furukawa, K. (1997) J. Biol. Chem. 272, 24794-24799). **Northern** analysis of mRNA from human organs with the four homologous cDNA revealed different **expression patterns**. beta3Gal-T1 mRNA was expressed in brain, beta3Gal-T2 was expressed in brain and heart, and beta3Gal-T3 and -T4 were more widely expressed. The coding regions for each of the four genes were contained in single exons. beta3Gal-T2, -T3, and -T4 were localized to 1q31, 3q25, and 6p21.3, respectively, by EST mapping. The results demonstrate the existence of a family of homologous beta3-galactosyltransferase genes.

L92 ANSWER 24 OF 36 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 1998137798 MEDLINE
DOCUMENT NUMBER: 98137798 PubMed ID: 9469939
TITLE: Cloning of a retinally abundant regulator of G-protein signaling (RGS-r/RGS16): genomic structure and chromosomal localization of the human gene.
COMMENT: Erratum in: Gene 1998 Jun 15;213(1-2):223
Erratum in: Gene 1998 Sep 14;217(1-2):187
AUTHOR: Snow B E; Antonio L; Suggs S; Siderovski D P
CORPORATE SOURCE: Quantitative Biology Laboratory, Amgen Institute, 620 University Avenue, M5G 2C1, Toronto, Ontario, Canada.
SOURCE: GENE, (1998 Jan 12) 206 (2) 247-53.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF009356; GENBANK-U94828; GENBANK-U94829
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980410
Last Updated on STN: 20000303
Entered Medline: 19980327

AB Regulators of G-protein signaling (RGS) constitute a family of GTPase-activating proteins with varying tissue-specific **expression patterns** and G-protein alpha subunit specificities. Here, we

describe the molecular cloning of the human RGS-r/RGS16 cDNA, encoding a predicted polypeptide of 23kDa that shows 86% identity to mouse RGS-r. **Northern** blot analysis shows that, like the mouse Rgs-r message, hRGS-r mRNA is abundantly expressed in retina, with lower levels of expression in most other tissues examined. Characterization of the genomic
organization of the hRGS-r gene shows that it consists of five exons and four introns. We have also mapped the human RGS-r /RGS16 gene to chromosome 1q25-1q31 by fluorescence in situ hybridzation. Analysis of human **ESTs** reveals that at least five members of the RGS gene family map to chromosome 1q, suggesting that at least part of the RGS family arose through gene duplication. The chromosomal location, retinal abundance, and presumed function of the human RGS-r protein in desensitizing photoreceptor signaling make the RGS-r/RGS16 locus a candidate for mutations responsible for retinitis pigmentosa with para-arteriolar preservation of retinal pigment epithelium (RP-PPRE or RP12), an autosomal recessive disorder previously mapped to 1q31.

L92 ANSWER 25 OF 36 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 1999014245 MEDLINE
DOCUMENT NUMBER: 99014245 PubMed ID: 9795190
TITLE: cDNA sequence analysis, chromosomal assignment and **expression pattern** of the gene coding for integral membrane protein 2B.
AUTHOR: Pittois K; Deleersnijder W; Merregaert J
CORPORATE SOURCE: Department of Biochemistry, Laboratory of Molecular Biotechnology, University of Antwerp, Universiteitsplein 1, B-2610, Wilrijk, Belgium.
SOURCE: GENE, (1998 Sep 14) 217 (1-2) 141-9.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U76253
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981117

AB The complete cDNA of the mouse integral membrane protein 2B gene (Itm2b) was determined by sequence analysis of expressed sequence tag (EST) clone L26775 and a clone isolated from a cDNA library of the osteogenic stromal cell line MN7 (Mathieu et al., 1992. Calcif. Tissue Int. 50, 362-371) and by 5' rapid amplification of cDNA ends (RACE). Alignment of different mouse **ESTs** confirmed the entire sequence. **Northern** blot analysis of different neonatal and adult mouse tissues showed that Itm2b is ubiquitously expressed. There are three mRNAs with different lengths in neonatal as well as in adult tissues, originating from alternative polyadenylation by usage of one consensus and two additional variant polyadenylation signals. The cDNA sequence of the human Itm2b homolog (ITM2B) was assembled using data from available human **ESTs** . Both the mouse and the human gene code for a protein of 266 amino acids (aa) that is homologous to a previously described integral membrane protein, Itm2A, of which the expression is restricted to osteo- and chondrogenic tissues. Itm2A and Itm2B belong to a family of type II integral membrane proteins, which contains a third member, Itm2C (Deleersnijder et al., 1996. J. Biol. Chem. 271, 19475-19482). The human ITM2B and mouse Itm2b genes were previously mapped as unknown **ESTs** to conserved syntenic regions Homo sapiens 13q12-13 and Mus musculus 14.

L92 ANSWER 26 OF 36 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 1998234542 MEDLINE
DOCUMENT NUMBER: 98234542 PubMed ID: 9570947
TITLE: Divergently transcribed overlapping genes expressed in liver and kidney and located in the 11p15.5 imprinted domain.
AUTHOR: Cooper P R; Smilinich N J; Day C D; Nowak N J; Reid L H; Pearsall R S; Reece M; Prawitt D; Landers J; Housman D E; Winterpacht A; Zabel B U; Pelletier J; Weissman B E; Shows T B; Higgins M J
CORPORATE SOURCE: Department of Human Genetics, Roswell Park Cancer Institute, Buffalo, New York 14263, USA.
CONTRACT NUMBER: CA63176 (NCI)
CA63333 (NCI)
HG00333 (NHGRI)
SOURCE: GENOMICS, (1998 Apr 1) 49 (1) 38-51.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AC001228; GENBANK-AF087428
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 20000512
Entered Medline: 19980625

AB Human chromosomal band 11p15.5 has been shown to contain genes involved in the development of several pediatric and adult tumors and in Beckwith-Wiedemann syndrome (BWS). Overlapping P1 artificial chromosome clones from this region have been used as templates for genomic sequencing in an effort to identify candidate genes for these disorders. PowerBLAST identified several matches with expressed sequence tags (**ESTs**) from fetal brain and liver cDNA libraries. **Northern** blot analysis indicated that two of the genes identified by these **ESTs** encode transcripts of 1-1.5 kb with predominant expression in fetal and adult liver and kidney. With RT-PCR and RACE, full-length transcripts were isolated for these two genes, with the largest open reading frames encoding putative proteins of 253 and 424 amino acids. Database comparison of the predicted amino acid sequence of the larger transcript indicated homology to integral membrane organic cation transporters; hence, we designate this gene ORCTL2 (organic cation transporter-like 2). An expressed sequence polymorphism provided evidence that the ORCTL2 gene exhibits "leaky" imprinting in both human fetal kidney and human fetal liver. The mouse orthologue (Orctl2) was identified, and a similar polymorphism was used to demonstrate maternal-specific expression of this gene in fetal liver from interspecific F1 mice. The predicted protein of the smaller gene showed no significant similarity in the database. **Northern** and RACE analyses suggest that this gene may have multiple transcription start sites. Determination of the genomic structure in humans indicated that the 5'-end of this transcript overlaps in divergent orientation with the first two exons of ORCTL2, suggesting a possible role for antisense regulation of one gene by the other. We, therefore, provisionally name this second transcript ORCTL2S (ORCTL2-antisense). The **expression patterns** of these genes and the imprinted expression of ORCTL2 are suggestive of a possible role in the development of Wilms tumor (WT) and hepatoblastoma. Although

SSCP analysis of 62 WT samples and 10 BWS patients did not result in the identification of any mutations in ORCTL2 or ORCTL2S, it will be important to examine their **expression pattern** in tumors and BWS patients, since epigenetic alteration at these loci may play a role in the etiology of these diseases.

L92 ANSWER 27 OF 36 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 1999077824 MEDLINE
DOCUMENT NUMBER: 99077824 PubMed ID: 9858671
TITLE: Fluorescent differential display analysis of gene expression in apoptotic neuroblastoma cells.
AUTHOR: Choi D K; Ito T; Mitsui Y; Sakaki Y
CORPORATE SOURCE: Human Genome Center, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108, Japan.
SOURCE: GENE, (1998 Nov 26) 223 (1-2) 21-31.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U63289
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 19990316
Entered Medline: 19990303

AB Identification of differentially expressed genes will provide leads in the elucidation of the molecular mechanisms underlying neuronal cell death associated with neurodegenerative disorders. Using a high-throughput fluorescent differential display (FDD) system based on an automated DNA sequencer, we analyzed global patterns of gene expression during the apoptosis of neuroblastoma SH-SY5Y cells induced by a neurotoxin, colchicine. Initial screening of approximately 24000 cDNA bands displayed with 320 primer combinations has revealed 263 fragments showing differential **expression patterns**, suggesting that approximately 1% of transcripts are modulated in their expression level. Of these differentially displayed bands, we cloned 18 fragments composed of 17 distinct species and confirmed differential expression of each species by reverse transcription-PCR or **Northern** blot hybridization, thereby proving the reliability of the approach. These include eight derived from seven known genes, five homologous to expressed sequence tags (**ESTs**), and five totally lacking any homology to those deposited in the database. Among these, a novel transcript SAI1 induced prominently was characterized further and revealed to encode a putative RNA-binding protein NAPOR (neuroblastoma apoptosis-related RNA-binding protein), containing three copies of evolutionarily conserved RNA recognition motif. Since several RNA-binding proteins have been known to play crucial roles in other apoptosis systems, it is conceivable that NAPOR is also involved in the process of neuronal cell death.

L92 ANSWER 28 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1997:226582 BIOSIS
DOCUMENT NUMBER: PREV199799518298
TITLE: Cloning of a human RNA editing deaminase (ADARB1) of glutamate receptors that maps to chromosome 21q22.3.
AUTHOR(S): Mittaz, Laureane; Scott, Hamish S.; Rossier, Colette; Seeburg, Peter H.; Higuchi, Miyoko; Antonarakis, Stylianos

E. (1)
CORPORATE SOURCE: (1) Div. Med. Genet., Dep. Genet. Microbiol., Univ. Geneva Med. Sch., 1 Rue Michel Servet, 1211 Geneva 4 Switzerland
SOURCE: Genomics, (1997) Vol. 41, No. 2, pp. 210-217. ISSN: 0888-7543.
DOCUMENT TYPE: Article
LANGUAGE: English
AB RED1 is a double-stranded RNA-specific editase characterized in the rat and is implicated in the editing of glutamate receptor subunit pre-mRNAs, particularly in the brain. Starting from human **ESTs** homologous to the rat RED1 sequence, we have characterized two forms of human RED1 cDNAs, one form coding for a putative peptide of 701 amino acids (similar to the shorter of two rat mRNAs) and a long form coding for a putative protein of 741 amino acids, the extra 120 bp of which are homologous to an AluJ sequence. Both forms were observed at approximately equal levels in cDNA clones and in seven different human tissues tested by RT-PCR. The human and rat short isoforms have 95 and 85% sequence identity at the amino acid and nucleotide levels, respectively. The human sequence (designated ADARB1 by the HGMW Nomenclature Committee) contains two double-stranded RNA-binding domains and a deaminase domain implicated in its editing action. **Northern** blot analysis detected two transcripts of 8.8 and 4.2 kb strongly expressed in brain and in many human adult and fetal tissues. ADARB1 maps to human chromosome 21q22.3, a region to which several genetic disorders map, including one form of bipolar affective disorder. Recently it was shown that heterozygous mice harboring an editing-incompetent glutamate receptor B allele have early onset fatal epilepsy. Since glutamate receptor channels are essential elements in synaptic function and plasticity and mediate pathology in many neurological disorders, and since RED1 is central in glutamate receptor channel control, ADARB1 is a candidate gene for diseases with neurological symptoms, such as bipolar affective disorder and epilepsy.

L92 ANSWER 29 OF 36 MEDLINE
ACCESSION NUMBER: 97420696 MEDLINE
DOCUMENT NUMBER: 97420696 PubMed ID: 9276681
TITLE: A survey of genes expressed in mouse embryonal carcinoma F9 cells: characterization of expressed sequence tags matching no known genes.
AUTHOR: Nomura M; Nishiguchi S; Motaleb M A; Takihara Y; Takagi T; Yasunaga T; Shimada K
CORPORATE SOURCE: Department of Medical Genetics, Research Institute for Microbial Diseases, Osaka University.
SOURCE: JOURNAL OF BIOCHEMISTRY, (1997 Jul) 122 (1) 129-47. Journal code: 0376600. ISSN: 0021-924X.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D21355; GENBANK-D21356; GENBANK-U21357; GENBANK-U21358; GENBANK-U21359; GENBANK-U21360; GENBANK-U21361; GENBANK-U21362; GENBANK-U21363; GENBANK-U21364; GENBANK-U21365; GENBANK-U21366; GENBANK-U21367; GENBANK-U21368; GENBANK-U21369; GENBANK-U21370; GENBANK-U21371; GENBANK-U21372; GENBANK-U21373; GENBANK-U21374; GENBANK-U21375; GENBANK-U21376; GENBANK-U21377; GENBANK-U21378;

GENBANK-U21379; GENBANK-U21380; GENBANK-U21381; GENBANK-U21382
ENTRY MONTH: 199710
ENTRY DATE: Entered STN: 19971021
Last Updated on STN: 19971021
Entered Medline: 19971006

AB We prepared 2,132 expressed sequence tags (**ESTs**) from undifferentiated mouse embryonal carcinoma F9 cells and found that 1,416 match known gene and/or protein sequences [Nishiguchi et al. (1996) J. Biochem. 119, 749-767]. To obtain information on the functions of the remaining 716 unidentified **ESTs** and to develop a system for characterizing **ESTs** matching no known genes, we analyzed their sequences by (i) repeated database searches, using the BLASTN, BLASTX, TBLASTX, and FASTA programs, (ii) using computer programs developed or modified for this work, such as the WFASTA, ORFTRNS, and MFASTA programs, together with the DBPROSITE and GRAIL programs, and (iii) examining the **expression patterns** of the corresponding mRNAs in F9 cells and several organs of adult mice, using the digoxigenin-labeled dot-blot method. We found that 216 of the 716 **ESTs** match known gene and/or protein sequences, and 307 show significant similarities to these sequences, with a Poisson p-value < 0.01. The strategy and usefulness of such analysis for characterizing unidentified **ESTs** are discussed.

L92 ANSWER 30 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1997:501071 BIOSIS
DOCUMENT NUMBER: PREV199799800274
TITLE: Novel genes mapping to the critical region of the 5q-syndrome.
AUTHOR(S): Boultwood, Jacqueline (1); Fidler, Carrie; Soularue, Pascal; Strickson, Amanda J.; Kostrzewa, Markus; Jaju, Rina J.; Cotter, Finbarr E.; Fairweather, Nick; Monaco, Antony P.; Mueller, Ulrich; Lovett, Michael; Jabs, Ethylin Wang; Auffray, Charles; Wainscoat, James S.
CORPORATE SOURCE: (1) Leukaemia Res. Fund Molecular Haematology Unit, Univ. Dep. Cellular Sci., John Radcliffe Hosp., Headington, Oxford OX3 9DU UK
SOURCE: Genomics, (1997) Vol. 45, No. 1, pp. 88-96. ISSN: 0888-7543.
DOCUMENT TYPE: Article
LANGUAGE: English

AB The 5q- syndrome is a myelodysplastic syndrome with specific hematological features and a good prognosis. Using molecular mapping techniques, we have previously defined the critical region of gene loss of the 5q- chromosome in the 5q- syndrome as the approximately 5-Mb region at 5q31-q33 flanked by the genes for FGF1 and IL12B. This region is completely represented by a series of overlapping YACs, and we are currently generating a transcription map with the aim of identifying the tumor-suppressor gene associated with the development of the 5q- syndrome. In this study two techniques have been used: first, the screening of full-length cDNA libraries with radiolabeled YACs and second, the mapping of chromosome 5-specific expressed sequence tags (**ESTs**) to a YAC contig. A 1-Mb YAC contig encompassing the CSF1R gene has been used to screen a fetal brain cDNA library, and this has resulted in the identification of two genes comprising one known gene previously localized to the region (ADRB2) and one known gene previously unlocalized. Six of 135 chromosome 5-specific **ESTs** were localized by PCR screening to the YAC contig mapping to the critical region of the 5q- syndrome. IMAGE cDNA

clones for each of the six **ESTs** have been obtained. These seven (excluding ADRB2) newly assigned cDNA clones were subjected to further analysis. The **expression patterns** of each of the cDNA clones have been established in a range of human tissues, including bone marrow. Six of seven cDNAs are expressed in human bone marrow. Six of seven cDNAs have no known homology to any deposited human sequences, and one (C29) is dihydropyrimidinase-related protein-3, a member of a novel gene family. Genomic localization and **expression patterns** would suggest that these newly assigned cDNAs represent potential candidate genes for the 5q- syndrome.

L92 ANSWER 31 OF 36 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 96375776 MEDLINE
DOCUMENT NUMBER: 96375776 PubMed ID: 8782065
TITLE: Identification of genes associated with myocardial development.
AUTHOR: Fung Y W; Liew C C
CORPORATE SOURCE: Department of Clinical Biochemistry, Toronto Hospital, University of Toronto, Canada.
SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1996 Jun) 28
(6) 1241-9.
Journal code: 0262322. ISSN: 0022-2828.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199611
ENTRY DATE: Entered STN: 19961219
Last Updated on STN: 19961219
Entered Medline: 19961127

AB We are conducting a cDNA sequencing project using human heart cDNA libraries to study expression of genes in the human heart. From our human heart cDNA libraries, we have accumulated over 10,000 partial cDNA sequences (expressed sequence tags-**ESTs**) representing both the previously uncharacterized and known transcripts expressed in the human heart (Liew et al., 1994). Currently, we have applied dot blot hybridization as a rapid approach to determine the genes putatively involved in myocardial development. Differential **expression patterns** of gene transcripts represented by the cDNA clones can be revealed by comparing dot intensities on the autoradiographs, after hybridization with cDNA probes generated from neonatal and adult heart mRNAs, cDNA clones (1505) have been processed by dot blot hybridization, of which 924 and 581 represented novel and known transcripts respectively.

Among the screened clones, about 1.4% were found to be differentially expressed during heart development. Further verification was accomplished by **Northern** blot analysis. By grouping the 581 clones corresponding to known transcripts, a study of the gene expression profile of the heart in the cardiovascular system can be achieved.

L92 ANSWER 32 OF 36 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 96319713 MEDLINE
DOCUMENT NUMBER: 96319713 PubMed ID: 8697448
TITLE: A novel profile of expressed sequence tags for zinc finger encoding genes from the poorly differentiated exocrine pancreatic cell line AR4IP.
AUTHOR: Gebelein B; Mesa K; Urrutia R
CORPORATE SOURCE: Department of Molecular Neuroscience, Mayo Clinic, Rochester, MN 55905, USA.

SOURCE: CANCER LETTERS, (1996 Aug 2) 105 (2) 225-31.
Journal code: 7600053. ISSN: 0304-3835.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U78129; GENBANK-U78130; GENBANK-U78131;
GENBANK-U78132; GENBANK-U78133; GENBANK-U78134;
GENBANK-U78135; GENBANK-U78136; GENBANK-U78137;
GENBANK-U78138; GENBANK-U78139; GENBANK-U78140;
GENBANK-U78141; GENBANK-U78142; GENBANK-U78143;
GENBANK-U78144; GENBANK-U78145; GENBANK-U78146
ENTRY MONTH: 199609
ENTRY DATE: Entered STN: 19960912
Last Updated on STN: 19980206
Entered Medline: 19960903

AB Genes encoding for C2H2 zinc finger proteins are known to regulate normal cell proliferation and differentiation and have often been found to be mutated in different forms of cancer. We are interested in understanding the role of these genes as regulators of cell proliferation and differentiation in the exocrine pancreas. Therefore, we have generated expressed sequence tags (**ESTs**) encoding pancreas-enriched zinc finger peptides using the polymerase chain reaction and hybridization techniques [Adams, M.D. et al. (1991) Science, 252, 1651-1656]. Here we report the primary structure and **expression pattern** of 18 different zinc finger-encoding cDNAs (DZF-1-18) from the azaserine-derived tumoral cell line AR4IP which displays a poorly differentiated phenotype. Sequence analysis shows that all of these clones encode peptides which share the consensus DNA-binding motif with the Drosophila zinc finger transcription factor kruppel. High stringency **Northern** blot analysis shows that eight different zinc finger transcripts are expressed at high levels in normal adult rat pancreas and therefore constitute good candidates to play a role as transcription factors in exocrine pancreatic cells.

L92 ANSWER 33 OF 36 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 96207310 MEDLINE
DOCUMENT NUMBER: 96207310 PubMed ID: 8617497
TITLE: Regional assignment and tissue expression of twenty-three expressed sequence tags (**ESTs**) from human chromosome 5.
AUTHOR: Feldblyum T V; Maglott D R; McPherson J D; Adams M; Apostol B L; Durkin A S; Wasmuth J J; Nierman W C
CORPORATE SOURCE: American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland, 20852, USA.
SOURCE: GENOMICS, (1996 Apr 1) 33 (1) 128-30.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199606
ENTRY DATE: Entered STN: 19960620
Last Updated on STN: 19960620
Entered Medline: 19960613

AB Regional localization and **expression patterns** are reported for 19 expressed sequence tags (**ESTs**) from human chromosome 5, two of which were derived from the same transcript. Two of the **ESTs** correspond to genes not previously characterized in

humans: a stress-activated protein kinase and nicotinamide nucleotide transhydrogenase. Expression was determined by three methods: **Northern** blots, PCR from tissue-specific cDNA libraries, and sequence sampling from EST sequencing projects. Six of the **ESTs** show no expression, and EST01986 appears to be expressed predominantly in the brain by all methods tested.

L92 ANSWER 34 OF 36 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 96236220 MEDLINE
DOCUMENT NUMBER: 96236220 PubMed ID: 8674973
TITLE: Quantitative analysis of gene expression in sexual structures of Aspergillus nidulans by sequencing of 3'-directed cDNA clones.
AUTHOR: Lee D W; Lee S H; Hwang H A; Kim J H; Chae K S
CORPORATE SOURCE: Department of Molecular Biology, Chonbuk Nation University,
Chonju, South Korea.
SOURCE: FEMS MICROBIOLOGY LETTERS, (1996 Apr 15) 138 (1) 71-6.
Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U41133; GENBANK-U41134; GENBANK-U41135; GENBANK-U41136; GENBANK-U41137; GENBANK-U41138; GENBANK-U41139; GENBANK-U41140; GENBANK-U41141; GENBANK-U41142; GENBANK-U41143; GENBANK-U41144; GENBANK-U41145; GENBANK-U41146; GENBANK-U41147; GENBANK-U41148; GENBANK-U41149; GENBANK-U41150; GENBANK-U41151; GENBANK-U41152; GENBANK-U41153; GENBANK-U41154; GENBANK-U41155; GENBANK-U41156; GENBANK-U41157; GENBANK-U41158; GENBANK-U41159; GENBANK-U41160; GENBANK-U41161
ENTRY MONTH: 199608
ENTRY DATE: Entered STN: 19960822
Last Updated on STN: 19960822
Entered Medline: 19960809
AB We constructed a 3'-directed cDNA library of cleistothecia and Hulle cells of Aspergillus nidulans to examine gene **expression patterns** of the sexual structures and to have probes necessary to isolate sexual structure-specific genes. Sequencing of 360 randomly selected cDNA clones yielded 272 expressed sequence tags (**ESTs**), most of which probably represent frequently or less expressed genes in sexual structures of A. nidulans. Among the 272 **ESTs**, 33 **ESTs** (87 cDNA clones) appeared more than once and 2 **ESTs** appeared 6 times; 9 **ESTs** matched GenBank entries. When compared with sequences obtained from a mycelial 3'-directed cDNA library of A. nidulans, 28 out of 33 **ESTs** seem to be sexual structure-specific. **Northern** blot analyses of 20 **ESTs** showed that 17 are sexual structure-specific. The remaining three **ESTs** also hybridized with RNA isolated from vegetative mycelia. These results suggest that analyses of **ESTs** from different cell types or tissues can readily demonstrate gene **expression patterns** of specific cell types and identify cell type-specific cDNA probes.

L92 ANSWER 35 OF 36 MEDLINE
ACCESSION NUMBER: 1998099668 MEDLINE
DOCUMENT NUMBER: 98099668 PubMed ID: 9238082
TITLE: Isolation of differentially expressed human fovea genes:

candidates for macular disease.
AUTHOR: Bernstein S L; Borst D E; Wong P W
CORPORATE SOURCE: National Eye Institute, National Institutes of Health, Bethesda, MD, USA.. slbernst@umabnet.ab.umd.edu
SOURCE: MOLECULAR VISION, (1995 Dec 21) 1 4.
Journal code: 9605351. ISSN: 1090-0535.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980618
Last Updated on STN: 19980618
Entered Medline: 19980611

AB PURPOSE: In humans, the fovea is the region of the retina responsible for acute vision. Disorders affecting the fovea are responsible for the majority of cases of untreated blindness in the developed world, yet are poorly understood at the molecular level. Our goal is to identify genes that are preferentially expressed within the human fovea as compared to the midperipheral retina (differential fovea clones). MATERIALS AND METHODS: An unamplified fovea cDNA library was differentially screened with cDNA probes derived from either human fovea or midperipheral retina. Rounds of secondary screening and **northern** analysis were used to verify the **expression pattern** of a selective number of clones isolated. RESULTS: Forty-one differential fovea clones were isolated from a screening of 10,000 phage clones (clones). Of these clones, 31.5 % correspond to known sequences present in GenBank/EMBL and 70.7% represent novel human fovea expressed sequence tags (**ESTs**). **Northern** analysis of selected clones demonstrated that they represent genes expressed at higher levels in the human fovea than in the midperipheral retina. CONCLUSIONS: Genes that are more highly expressed in the fovea as opposed to the midperipheral retina are likely to represent essential genes for fovea function. Using our fovea cDNA library, we are able to isolate differential human fovea clones at an incidence of 41/10,000 clones screened. We demonstrate that there is a high level of differential gene expression within different regions of the human retina.

L92 ANSWER 36 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1994:400086 BIOSIS
DOCUMENT NUMBER: PREV199497413086
TITLE: Cloning and characterization of pig muscle cDNAs by an expressed sequence tag approach.
AUTHOR(S): Tuggle, C. K.; Schmitz, C. B.
CORPORATE SOURCE: Dep. Anim. Sci., Iowa State Univ., Ames, IA 50011 USA
SOURCE: Animal Biotechnology, (1994) Vol. 5, No. 1, pp. 1-13.
ISSN: 1049-5398.
DOCUMENT TYPE: Article
LANGUAGE: English

AB To provide additional unique marker sequences for genome mapping, we have cloned and partially sequenced 14 pig skeletal muscle cDNAS, representing 11 independent genes. Random selection from an adult skeletal muscle cDNA library, coupled with dot blot hybridization of the cDNA clones with complex probes representing muscle and non-muscle gene expression, was used to identify putative muscle-specific cDNAs. These cDNAs were then partially sequenced and the resulting primary structural information was used to screen the Genbank/European Molecular Biology Laboratory (EMBL) and Protein Information Resource (PIR) databases. Pig cDNAs with significant similarity to alpha-actin, alpha-7-integrin, alpha-actinin2, myosin binding protein H, and myosin light chain kinase were identified.

Northern analysis of alpha-actinin2 showed the **expression pattern** of this pig gene closely matched that reported for human alpha-actinin2. Six cDNAs had no significant database match indicating that these genes have not been sequenced in other species. These new pig **ESTs** can be physically and genetically mapped for use in comparative genome mapping, and will be useful in the genetic and biochemical analysis of muscle.

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=> d history

     (FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

     FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
     ON 08 JUL 2002
L1         13496 S EST
L2            34 S L1(S)(NO#(W)CORRELAT?)
L3            21 DUP REM L2 (13 DUPLICATES REMOVED)
L4          3375 S L1(S)(MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5          1972 S L4(S)(PROTEIN OR PEPTIDE)
L6          1748 S L5(S)(EXPRESS?)
L7           775 S L6(S)DATABASE#
L8           355 DUP REM L7 (420 DUPLICATES REMOVED)
L9            96 S L8(S)(PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10           47 S L8(S)GENBANK
L11           87 S L8(S)(HEART OR BONE OR BRAIN)
L12          137 S L11 OR L9
L13            1 S L12 AND (NO#(W)EXPRESS?)
L14           67 S L12(S)(TRANSCRI?)
L15           86 S L8(S)NORTHERN
L16           50 S L1(S)(NO#(2W)CORRELAT?)
L17           16 S L16 NOT L2
L18           12 DUP REM L17 (4 DUPLICATES REMOVED)
L19           54 S L1(S)(NO#(3W)CORRELAT?)
L20            0 S L19 NOT L1
L21           20 S L19 NOT L2
L22            4 S L21 NOT L16

     FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002
L23        13496 S EST OR (SEQUENCE(W)TAG#)
L24          234 S L23 AND DATABASE#/TI
L25            0 S L24 AND (NO(3W)CORRELAT?)
L26          234 S L24(S)DATABASE#
L27         2221 S L23(S)DATABASE#
L28            4 S L27(S)(NO#(3W)CORRELAT?)
L29         1174 S L23(S)(BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30          310 S L29(S)NORTHERN
L31          133 S L30 AND DATABASE#
L32           78 DUP REM L31 (55 DUPLICATES REMOVED)
L33         1072 S L23(S)(PREDICT? OR ANTICIPAT?)
L34           22 S L33 AND DATABASE#/TI
L35           13 DUP REM L34 (9 DUPLICATES REMOVED)
L36           22 S L34(S)DATABASE#
L37         2221 S L23(S)DATABASE#
L38          612 S L37(S)TISSUE
L39           58 S L38(S)PROSTATE
L40           10 S L39 AND PREDICT?
L41            6 DUP REM L40 (4 DUPLICATES REMOVED)
L42            1 S L23(S)(CANNOT(3W)PREDICT)
L43        13596 S L23 OR DBEST
```

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L44         6719 S L43(S)EXPRESS?
L45          192 S L44(S)BLAST
L46           47 S L45(S)PREDICT?
L47           27 DUP REM L46 (20 DUPLICATES REMOVED)
L48            2 S L43(S)RELIED
L49            1 S L43(S)(("NOT" OR CANNOT)(W)PREDICT?)
L50            0 S L43(S)(CANNOT(W)ANTICIPATE)
L51          797 S L43(S)TRANSCRIPTS
L52           28 S L43(S)((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
L53           17 DUP REM L52 (11 DUPLICATES REMOVED)
L54          546 S L43 AND (EXPRESSION(A)PATTERN#)
L55           15 S L54 AND DATABASE#/TI
L56            9 DUP REM L55 (6 DUPLICATES REMOVED)
L57          239 S L43 AND DATABASE#/TI
L58            5 S L57 AND PREDICT
L59            3 DUP REM L58 (2 DUPLICATES REMOVED)
L60         1735 S L43(S)LIBRAR?
L61           34 S L60(S)PREDICT
L62           19 DUP REM L61 (15 DUPLICATES REMOVED)
L63         4276 S L43(S)(MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
L64          335 S L63(S)(EXPRESSION(A)PATTERN#)
L65           86 S L64(S)(PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L66           49 DUP REM L65 (37 DUPLICATES REMOVED)
L67          430 S L43(S)(EXPRESSION(A)PATTERN#)
L68           12 S L67 AND DATABASE#/TI
L69            6 DUP REM L68 (6 DUPLICATES REMOVED)
L70           99 S L23(3A)PREDICT?
L71            2 S L70(3A)(EXPRESSION OR TRANSCRIPTION)
L72          152 S L43(5A)PREDICT?
L73            3 S L72(5A)(EXPRESSION OR TRANSCRIPTION)
L74            1 S L73 NOT L71
L75           64 S L43(S)HYPOTHETICAL
L76           55 S L75(S)(EXPRESS? OR TRANSCI?)
L77           34 DUP REM L76 (21 DUPLICATES REMOVED)
L78           28 S L30(S)(EXPRESSION(A)PATTERN#)
L79           15 DUP REM L78 (13 DUPLICATES REMOVED)
L80            0 S L23(S)("NOT"(W)PREDICTIVE)
L81            0 S L23(S)(CANNOT(W)ANTICIPATE)
L82          107 S DATABASE(A)MINING
L83           14 S L23 AND L82
L84            8 DUP REM L83 (6 DUPLICATES REMOVED)
L85         2347 S ESTS
L86           79 S L85 AND DATABASE/TI
L87            0 S L86 AND (CANNOT(W)(ANTICIPATE OR PREDICT))
L88            4 S L86 AND (EXPRESSION(A)PATTERN#)
L89            2 DUP REM L88 (2 DUPLICATES REMOVED)
L90          331 S L85 AND NORTHERN
L91           58 S L90 AND (EXPRESSION(A)PATTERN#)
L92           36 DUP REM L91 (22 DUPLICATES REMOVED)

=> s l23(s)(cannot(5a)predict?)
L93            3 L23(S)(CANNOT(5A) PREDICT?)

=> d ibib abs tot

L93  ANSWER 1 OF 3     MEDLINE
ACCESSION NUMBER:   2002172902     IN-PROCESS
DOCUMENT NUMBER:    21859662   PubMed ID: 11870237
TITLE:              High frequency of DAZ1/DAZ2 gene deletions in patients
with
                    severe oligozoospermia.
```

AUTHOR: Fernandes S; Huellen K; Goncalves J; Dukal H; Zeisler J; Rajpert De Meyts E; Skakkebaek N E; Habermann B; Krause W; Sousa M; Barros A; Vogt P H

CORPORATE SOURCE: Reproduction Genetics, Institute of Human Genetics, University of Heidelberg, Heidelberg, Germany.

SOURCE: MOLECULAR HUMAN REPRODUCTION, (2002 Mar) 8 (3) 286-98. Journal code: 9513710. ISSN: 1360-9947.

PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals

ENTRY DATE: Entered STN: 20020322
Last Updated on STN: 20020322

AB Deletions of the DAZ gene family in distal Yq11 are always associated with deletions of the azoospermia factor c (AZFc) region, which we now estimate extends to 4.94 Mb. Because more Y gene families are located in this chromosomal region, and are expressed like the DAZ gene family only in the male germ line, the testicular pathology associated with complete AZFc deletions **cannot predict** the functional contribution of the DAZ gene family to human spermatogenesis. We therefore established a DAZ gene copy specific deletion analysis based on the DAZ-BAC sequences in GenBank. It includes the deletion analysis of eight DAZ-DNA PCR markers [six DAZ-single nucleotide varients (SNVs) and two DAZ-**sequence tag** sites (STS)] selected from the 5' to the 3'end of each DAZ gene and a deletion analysis of the gene copy specific EcoRV and TaqI restriction fragments identified in the internal repetitive DAZ gene regions (DYS1 locus). With these diagnostic tools, 63 DNA samples from men with idiopathic oligozoospermia and 107 DNA samples from men with proven fertility were analysed for the presence of the complete DAZ gene locus, encompassing the four DAZ gene copies. In five oligozoospermic patients, we found a DAZ-SNV/STS and DYS1/EcoRV and TaqI fragment deletion pattern indicative for deletion of the DAZ1 and DAZ2 gene copies; one of these deletions could be identified as a 'de-novo' deletion because it was absent in the DAZ locus of the patient's father. The same DAZ deletions were not found in any of the 107 fertile control samples. We therefore conclude that the deletion of the DAZ1/DAZ2 gene doublet in five out of our 63 oligozoospermic patients (8%) is responsible for the patients' reduced sperm numbers. It is most likely caused by intrachromosomal recombination events between two long repetitive sequence blocks (AZFc-Rep1) flanking the DAZ gene structures.

L93 ANSWER 2 OF 3 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:199005 BIOSIS

DOCUMENT NUMBER: PREV200200199005

TITLE: The transcriptome of bone marrow cells in chronic leukemias.

AUTHOR(S): Silva, Wilson A., Jr. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago, Marco A. (1)

CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 550a-551a. http://www.bloodjournal.org/. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11,

2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The complete collection of transcripts generated from the human genome **cannot** be **predicted** from the genome sequence, but should be directly determined for each tissue, due to variations of gene expression in different tissues and disease states, and because genes can encode multiple transcripts derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million expressed **sequence tags** (**EST**) from different cancer tissues, we constructed a set of cDNAs obtained from bone marrow cells of patients with CML and CLL, that represent partial expressed gene sequences that are biased toward the central coding regions of the resulting transcripts (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000). The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, protein metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative proteins with unknown functions, DNA clones orthologs and paralogs, whereas 852 were classified as no hits. The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in bone marrow cells was compared with other normal and neoplastic tissues from breast, prostate, colon, and brain. Of the 10 larger contigs, 5 genes were commonly expressed in most of the other tissues, one was exclusively found in bone marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in bone marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing protein, beta-globin and Xg antigen. Among 852 contigs that did not match annotated regions of the genome (no hits), the predicted protein sequence of 77 contigs matched known protein domains when evaluated by pfam (protein family database of alignment and HMMs), representing candidate unannoted genes. To search for single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies SMPs by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat Genet 23:452, 1999). A total of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealthy of information provided by this approach demonstrates its usefulness for the analysis of gene expression in specific hematopoietic tissues and diseases.

L93 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151895 BIOSIS
DOCUMENT NUMBER: PREV200200151895
TITLE: The transcriptome of bone marrow cells in chronic leukemia.

AUTHOR(S): Silva-Junior, Wilson A. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago, Marco A.
CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 131b. http://www.bloodjournal.org/. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The complete collection of transcripts generated from the human genome **cannot** be **predicted** from the genome sequence, but should be directly determined for each tissue, due to variations of gene expression in different tissues and disease states, and because genes can encode multiple transcripts derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million expressed **sequence tags** (**EST**) from different cancer tissues, we constructed a set of cDNAs obtained from bone marrow cells of patients with CML and CLL, that represent partial expressed gene sequences that are biased toward the central coding regions of the resulting transcripts (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000), The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, protein metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative proteins with unknown functions, DNA clones, orthologs and paralogs, whereas 852 were classified as no hits. The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in bone marrow cells was compared with other normal and neoplastic tissues from breast, prostate, colon, and brain. Of the 10 larger contigs, 5 genes were commonly expressed in most of the other tissues, one was exclusively found in bone marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in bone marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing protein, beta-globin and Xg antigen. Among 852 contigs that did not match annotated regions of the genome (no hits), the predicted protein sequence of 77 contigs matched known protein domains when evaluated by pfam (protein family database of alignment and HMMs), representing candidate unannoted genes. To search for single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies SNPs by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat Genet 23:452, 1999). A total

of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealthy of information provided by this approach demonstrates its usefulness for the analysis of gene expression in specific hematopoietic tissues and diseases.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT 19:04:09
ON 08 JUL 2002

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L1         13496 S EST
L2            34 S L1(S)(NO#(W)CORRELAT?)
L3            21 DUP REM L2 (13 DUPLICATES REMOVED)
L4          3375 S L1(S)(MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5          1972 S L4(S)(PROTEIN OR PEPTIDE)
L6          1748 S L5(S)(EXPRESS?)
L7           775 S L6(S)DATABASE#
L8           355 DUP REM L7 (420 DUPLICATES REMOVED)
L9            96 S L8(S)(PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10           47 S L8(S)GENBANK
L11           87 S L8(S)(HEART OR BONE OR BRAIN)
L12          137 S L11 OR L9
L13            1 S L12 AND (NO#(W)EXPRESS?)
L14           67 S L12(S)(TRANSCRI?)
L15           86 S L8(S)NORTHERN
L16           50 S L1(S)(NO#(2W)CORRELAT?)
L17           16 S L16 NOT L2
L18           12 DUP REM L17 (4 DUPLICATES REMOVED)
L19           54 S L1(S)(NO#(3W)CORRELAT?)
L20            0 S L19 NOT L1
L21           20 S L19 NOT L2
L22            4 S L21 NOT L16
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FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

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L24          234 S L23 AND DATABASE#/TI
L25            0 S L24 AND (NO(3W)CORRELAT?)
L26          234 S L24(S)DATABASE#
L27         2221 S L23(S)DATABASE#
L28            4 S L27(S)(NO#(3W)CORRELAT?)
L29         1174 S L23(S)(BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30          310 S L29(S)NORTHERN
L31          133 S L30 AND DATABASE#
L32           78 DUP REM L31 (55 DUPLICATES REMOVED)
L33         1072 S L23(S)(PREDICT? OR ANTICIPAT?)
L34           22 S L33 AND DATABASE#/TI
L35           13 DUP REM L34 (9 DUPLICATES REMOVED)
L36           22 S L34(S)DATABASE#
L37         2221 S L23(S)DATABASE#
L38          612 S L37(S)TISSUE
L39           58 S L38(S)PROSTATE
L40           10 S L39 AND PREDICT?
L41            6 DUP REM L40 (4 DUPLICATES REMOVED)
L42            1 S L23(S)(CANNOT(3W)PREDICT)
L43        13596 S L23 OR DBEST
L44         6719 S L43(S)EXPRESS?
```

```
L45          192 S L44(S)BLAST
L46           47 S L45(S)PREDICT?
L47           27 DUP REM L46 (20 DUPLICATES REMOVED)
L48            2 S L43(S)RELIED
L49            1 S L43(S)(("NOT" OR CANNOT)(W)PREDICT?)
L50            0 S L43(S)(CANNOT(W)ANTICIPATE)
L51          797 S L43(S)TRANSCRIPTS
L52           28 S L43(S)((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
L53           17 DUP REM L52 (11 DUPLICATES REMOVED)
L54          546 S L43 AND (EXPRESSION(A)PATTERN#)
L55           15 S L54 AND DATABASE#/TI
L56            9 DUP REM L55 (6 DUPLICATES REMOVED)
L57          239 S L43 AND DATABASE#/TI
L58            5 S L57 AND PREDICT
L59            3 DUP REM L58 (2 DUPLICATES REMOVED)
L60         1735 S L43(S)LIBRAR?
L61           34 S L60(S)PREDICT
L62           19 DUP REM L61 (15 DUPLICATES REMOVED)
L63         4276 S L43(S)(MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
L64          335 S L63(S)(EXPRESSION(A)PATTERN#)
L65           86 S L64(S)(PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L66           49 DUP REM L65 (37 DUPLICATES REMOVED)
L67          430 S L43(S)(EXPRESSION(A)PATTERN#)
L68           12 S L67 AND DATABASE#/TI
L69            6 DUP REM L68 (6 DUPLICATES REMOVED)
L70           99 S L23(3A)PREDICT?
L71            2 S L70(3A)(EXPRESSION OR TRANSCRIPTION)
L72          152 S L43(5A)PREDICT?
L73            3 S L72(5A)(EXPRESSION OR TRANSCRIPTION)
L74            1 S L73 NOT L71
L75           64 S L43(S)HYPOTHETICAL
L76           55 S L75(S)(EXPRESS? OR TRANSCI?)
L77           34 DUP REM L76 (21 DUPLICATES REMOVED)
L78           28 S L30(S)(EXPRESSION(A)PATTERN#)
L79           15 DUP REM L78 (13 DUPLICATES REMOVED)
L80            0 S L23(S)("NOT"(W)PREDICTIVE)
L81            0 S L23(S)(CANNOT(W)ANTICIPATE)
L82          107 S DATABASE(A)MINING
L83           14 S L23 AND L82
L84            8 DUP REM L83 (6 DUPLICATES REMOVED)
L85         2347 S ESTS
L86           79 S L85 AND DATABASE/TI
L87            0 S L86 AND (CANNOT(W)(ANTICIPATE OR PREDICT))
L88            4 S L86 AND (EXPRESSION(A)PATTERN#)
L89            2 DUP REM L88 (2 DUPLICATES REMOVED)
L90          331 S L85 AND NORTHERN
L91           58 S L90 AND (EXPRESSION(A)PATTERN#)
L92           36 DUP REM L91 (22 DUPLICATES REMOVED)
L93            3 S L23(S)(CANNOT(5A)PREDICT?)

=> s l23(s)(expression(a)pattern#)
L94          420 L23(S)(EXPRESSION(A) PATTERN#)

=> s l94(s)(cannot(5a)(predict or anticipate)
UNMATCHED LEFT PARENTHESIS 'S)(CANNOT'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> log hj
'HJ' IS NOT VALID HERE
For an explanation, enter "HELP LOGOFF".
```

```
=> log h
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                   293.79     610.50

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 22:59:26 ON 08 JUL 2002


Welcome to STN International!  Enter x:x

LOGINID:ssspta1600kxc

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Jan 25  BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS  3  Jan 29  FSTA has been reloaded and moves to weekly updates
 NEWS  4  Feb 01  DKILIT now produced by FIZ Karlsruhe and has a new update
                  frequency
 NEWS  5  Feb 19  Access via Tymnet and SprintNet Eliminated Effective 3/31/02
 NEWS  6  Mar 08  Gene Names now available in BIOSIS
 NEWS  7  Mar 22  TOXLIT no longer available
 NEWS  8  Mar 22  TRCTHERMO no longer available
 NEWS  9  Mar 28  US Provisional Priorities searched with P in CA/CAplus
                  and USPATFULL
 NEWS 10  Mar 28  LIPINSKI/CALC added for property searching in REGISTRY
 NEWS 11  Apr 02  PAPERCHEM no longer available on STN.  Use PAPERCHEM2
instead.
 NEWS 12  Apr 08  "Ask CAS" for self-help around the clock
 NEWS 13  Apr 09  BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS 14  Apr 09  ZDB will be removed from STN
 NEWS 15  Apr 19  US Patent Applications available in IFICDB, IFIPAT, and
IFIUDB
 NEWS 16  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and
ZCAPLUS
 NEWS 17  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22  Federal Research in Progress (FEDRIP) now available
 NEWS 19  Jun 03  New e-mail delivery for search results now available
 NEWS 20  Jun 10  MEDLINE Reload
 NEWS 21  Jun 10  PCTFULL has been reloaded
 NEWS 22  Jul 02  FOREGE no longer contains STANDARDS file segment

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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FILE 'HOME' ENTERED AT 11:50:48 ON 09 JUL 2002

=> file medline biosis

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FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 11:51:25 ON 09 JUL 2002

FILE 'BIOSIS' ENTERED AT 11:51:25 ON 09 JUL 2002
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=> s est# or (sequence(w)tag#)
L1 14581 EST# OR (SEQUENCE(W) TAG#)

=> s l1(s)("not" or cannot)
L2 83 L1(S)("NOT" OR CANNOT)

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 55 DUP REM L2 (28 DUPLICATES REMOVED)

=> d ibib abs tot

L3 ANSWER 1 OF 55 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002253113 MEDLINE
DOCUMENT NUMBER: 21988109 PubMed ID: 11861648
TITLE: A mouse serine protease TESP5 is selectively included into lipid rafts of sperm membrane presumably as a glycosylphosphatidylinositol-anchored protein.
AUTHOR: Honda Arata; Yamagata Kazuo; Sugiura Shin; Watanabe Katsuto; Baba Tadashi
CORPORATE SOURCE: Institute of Applied Biochemistry, University of Tsukuba, Tsukuba Science City, Ibaraki 305-8572, Japan.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 May 10) 277 (19) 16976-84.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB059414; GENBANK-AB059415
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020507
Last Updated on STN: 20020614
Entered Medline: 20020613

AB We have previously indicated that at least in mouse, sperm serine protease(s) other than acrosin probably act on the limited proteolysis of egg zona pellucida to create a penetration pathway for motile sperm, although the participation of acrosin **cannot** be ruled out completely. A 42-kDa gelatin-hydrolyzing serine protease present in mouse

sperm is a candidate enzyme involved in the sperm penetration of the zona pellucida. In this study, we have PCR-amplified an **EST** clone encoding a testicular serine protease, termed TESP5, and then screened a mouse genomic DNA library using the DNA fragment as a probe. The DNA sequence of the isolated genomic clones indicated that the TESP5 gene is identical to the genes coding for testicular testisin and eosinophilic esp-1. Immunochemical analysis using affinity-purified anti-TESP5 antibody revealed that 42- and 41-kDa forms of TESP5 with the isoelectric points of 5.0 to 5.5 are localized in the head, cytoplasmic droplet, and midpiece of cauda epididymal sperm probably as a membranous protein. Moreover, these two forms of TESP5 were selectively included into Triton X-100-insoluble microdomains, lipid rafts, of the sperm membranes. These results show the identity between TESP5/testisin/esp-1 and the 42-kDa sperm serine protease. When HEK293 cells were transformed by an expression plasmid carrying the entire protein-coding region of TESP5, the recombinant protein produced was released from the cell membrane by treatment with Bacillus cereus phosphatidylinositol-specific phospholipase C, indicating that TESP5 is glycosylphosphatidylinositol-anchored on the cell surface. Enzymatic properties of recombinant TESP5 was similar to but distinguished from those of rat acrosin and pancreatic trypsin by the substrate specificity and inhibitory effects of serine protease inhibitors.

L3 ANSWER 2 OF 55 MEDLINE
ACCESSION NUMBER: 2002172902 IN-PROCESS
DOCUMENT NUMBER: 21859662 PubMed ID: 11870237
TITLE: High frequency of DAZ1/DAZ2 gene deletions in patients with severe oligozoospermia.
AUTHOR: Fernandes S; Huellen K; Goncalves J; Dukal H; Zeisler J; Rajpert De Meyts E; Skakkebaek N E; Habermann B; Krause W; Sousa M; Barros A; Vogt P H
CORPORATE SOURCE: Reproduction Genetics, Institute of Human Genetics, University of Heidelberg, Heidelberg, Germany.
SOURCE: MOLECULAR HUMAN REPRODUCTION, (2002 Mar) 8 (3) 286-98. Journal code: 9513710. ISSN: 1360-9947.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020322
Last Updated on STN: 20020322

AB Deletions of the DAZ gene family in distal Yq11 are always associated with deletions of the azoospermia factor c (AZFc) region, which we now estimate extends to 4.94 Mb. Because more Y gene families are located in this chromosomal region, and are expressed like the DAZ gene family only in the male germ line, the testicular pathology associated with complete AZFc deletions **cannot** predict the functional contribution of the DAZ gene family to human spermatogenesis. We therefore established a DAZ gene copy specific deletion analysis based on the DAZ-BAC sequences in GenBank. It includes the deletion analysis of eight DAZ-DNA PCR markers [six DAZ-single nucleotide varients (SNVs) and two DAZ-**sequence tag** sites (STS)] selected from the 5' to the 3'end of each DAZ gene and a deletion analysis of the gene copy specific EcoRV and TaqI

restriction fragments identified in the internal repetitive DAZ gene regions (DYS1 locus). With these diagnostic tools, 63 DNA samples from men with idiopathic oligozoospermia and 107 DNA samples from men with proven fertility were analysed for the presence of the complete DAZ gene locus, encompassing the four DAZ gene copies. In five oligozoospermic patients, we found a DAZ-SNV/STS and DYS1/EcoRV and TaqI fragment deletion pattern indicative for deletion of the DAZ1 and DAZ2 gene copies; one of these deletions could be identified as a 'de-novo' deletion because it was absent in the DAZ locus of the patient's father. The same DAZ deletions were not found in any of the 107 fertile control samples. We therefore conclude that the deletion of the DAZ1/DAZ2 gene doublet in five out of our 63 oligozoospermic patients (8%) is responsible for the patients' reduced sperm numbers. It is most likely caused by intrachromosomal recombination events between two long repetitive sequence blocks (AZFc-Rep1) flanking the DAZ gene structures.

L3 ANSWER 3 OF 55 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002132649 MEDLINE
DOCUMENT NUMBER: 21686134 PubMed ID: 11827943
TITLE: Combining mouse congenic strains and microarray gene expression analyses to study a complex trait: the NOD model of type 1 diabetes.
AUTHOR: Eaves Iain A; Wicker Linda S; Ghandour Ghassan; Lyons Paul A; Peterson Laurence B; Todd John A; Glynne Richard J
CORPORATE SOURCE: Juvenile Diabetes Research Foundation/ Wellcome Trust Diabetes and Inflammation Laboratory, Cambridge Institute for Medical Research, University of Cambridge, Wellcome Trust/Medical Research Council Building, Addenbrooke's Hospital, Cambridge, CB2 2XY, UK.
SOURCE: GENOME RESEARCH, (2002 Feb) 12 (2) 232-43.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020301
Last Updated on STN: 20020315
Entered Medline: 20020314

AB Combining congenic mapping with microarray expression profiling offers an opportunity to establish functional links between genotype and phenotype for complex traits such as type 1 diabetes (T1D). We used high-density oligonucleotide arrays to measure the relative expression levels of >39,000 genes and **ESTs** in the NOD mouse (a murine model of T1D and other autoimmune conditions), four NOD-derived diabetes-resistant congenic strains, and two nondiabetic control strains. We developed a simple, yet general, method for measuring differential expression that provides an objective assessment of significance and used it to identify >400 gene expression differences and eight new candidates for the Idd9.1 locus. We also discovered a potential early biomarker for autoimmune hemolytic anemia that is based on different levels of erythrocyte-specific transcripts in the spleen. Overall, however, our results suggest that the dramatic disease protection conferred by six Idd loci (Idd3, Idd5.1, Idd5.2, Idd9.1, Idd9.2, and Idd9.3) **cannot** be rationalized in terms of global effects on the noninduced immune system. They also illustrate the degree to which regulatory systems appear to be robust to genetic variation. These observations have important implications for the design of future microarray-based studies in T1D and, more generally, for

studies that aim to combine genome-wide expression profiling and congenic mapping.

L3 ANSWER 4 OF 55 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002004287 MEDLINE
DOCUMENT NUMBER: 21624809 PubMed ID: 11752289
TITLE: PALS db: Putative Alternative Splicing database.
AUTHOR: Huang Y-H; Chen Y-T; Lai J-J; Yang S-T; Yang U-C
CORPORATE SOURCE: Bioinformatics Program, National Yang-Ming University, No. 155, Sec. 2, Li-Noun Street, Taipei, Taiwan 11221, Republic of China.
SOURCE: NUCLEIC ACIDS RESEARCH, (2002 Jan 1) 30 (1) 186-90. Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20020102
Last Updated on STN: 20020125
Entered Medline: 20020121

AB PALS db is a collection of Putative Alternative Splicing information from 19 936 human UniGene clusters and 16 615 mouse UniGene clusters. Alternative splicing (AS) sites were predicted by using the longest messenger RNA (mRNA) sequence in each UniGene cluster as the reference sequence. This sequence was aligned with related sequences in UniGene and dbEST to reveal the AS. This information was presented with six features: (i) literature aliases were used to improve the result of a gene name search; (ii) the quality of a prediction can be easily judged from the color-coded similarity and the scaled length of an alignment; (iii) we have clustered those **EST** sequences that support the same AS site together to enhance the users' confidence on a prediction; (iv) the users can also set up the alignment criteria interactively to recover false negatives; (v) tissue distribution can be displayed by placing the mouse cursor over an alignment; (vi) gene features will be analyzed at foreign sites by submitting the selected mRNA or its encoded protein as a query. Using these features, the users **cannot** only discover putative AS sites in silico, but also make new observations by combining AS information with tissue distributions or with gene features. PALS db is available at http://palsdb.ym.edu.tw/.

L3 ANSWER 5 OF 55 MEDLINE
ACCESSION NUMBER: 2002340016 IN-PROCESS
DOCUMENT NUMBER: 21932463 PubMed ID: 11934522
TITLE: Effects of frequency of treatment with recombinant equine somatotropin on selected biological responses in geldings.
AUTHOR: Thatcher C E; Thompson D L Jr
CORPORATE SOURCE: Department of Animal Science, Louisiana Agricultural Experiment Station, LSU Agricultural Center, Baton Rouge, LA, USA.
SOURCE: DOMESTIC ANIMAL ENDOCRINOLOGY, (2002 May) 22 (3) 127-43. Journal code: 8505191. ISSN: 0739-7240.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020627
Last Updated on STN: 20020627

AB Two experiments compared the efficacies of different treatment frequencies

for recombinant equine somatotropin (**eST**). In Experiment 1, five geldings received daily injections of **eST** at 20 microg/kg of body weight, and five received every-other-day injections at 40 microg/kg of body weight, for a total of 30 days. Plasma glucose (P=0.0001), insulin (P=0.0135), and non-esterified fatty acid (NEFA, P=0.0001) concentrations increased, and plasma urea nitrogen (PUN) concentrations decreased (P=0.0001), in both groups, and only minor differences (P<0.05) occurred between the two groups. Insulin-like growth factor-I (IGF-I) concentrations increased (P=0.0001) in both groups over time, and were higher (P<0.05) after day 2 in geldings treated daily. Endogenous somatotropin (ST) response to secretagogue was inhibited (P<0.05) in geldings receiving daily injections relative to those receiving every-other-day injections. In Experiment 2, 16 geldings were allotted to four groups of four. A control group received daily saline injections, and the other three groups received **eST** at 20 microg/kg of body weight daily as a single injection, two injections (every 12h), or four injections (every 6h), for a total of 14 days. Plasma IGF-I and insulin concentrations increased (P<0.05) in all groups receiving **eST**, with the responses being proportional to injection frequency. In contrast, PUN concentrations decreased (P<0.05) in all groups equally. In conclusion, the efficacy of daily versus every-other-day injections of **eST** depends upon the response to be measured, and for IGF-I concentrations, the every-other-day regimen was not acceptable. Injection frequencies greater than once daily were more efficacious for IGF-I and insulin concentrations, but not for PUN concentrations. Thus, the optimum injection regimen for any new application for **eST cannot** simply be inferred from other biological responses, and will need to be determined empirically.

L3 ANSWER 6 OF 55 MEDLINE
ACCESSION NUMBER: 2002296571 IN-PROCESS
DOCUMENT NUMBER: 22032956 PubMed ID: 12036583
TITLE: Characterization and in silico mapping of a novel murine zinc finger transcription factor.
AUTHOR: Wride Michael A; Mansergh Fiona C; Somani Jamila M; Winkfein Robert J; Rancourt Derrick E
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Calgary, 3330 Hospital Drive N.W., T2N 4N1, Calgary, AB, Canada.
SOURCE: GENE, (2002 May 1) 289 (1-2) 49-59.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020531
Last Updated on STN: 20020531

AB Transcription factors play important roles in development and homeostasis. We have completed an embryonic stem cell-based neural differentiation screen, which was carried out with a view to isolating early regulators of neurogenesis. Fifty eight of the expressed **sequence tags** isolated from this screen represent known transcription factors or sequences containing transcription factor motifs. We have determined the full-length sequence of a novel mouse zinc finger-containing gene (ZFEND; also known as Mus musculus zinc finger protein 358 (Zfp358)) that was identified from this screen. ZFEND has 87% nucleotide and 86% amino acid

identity to a previously identified human cDNA, FLJ10390, which is moderately similar to zinc finger protein 135. Northern blotting and RPAs demonstrate highest expression of ZFEND during mid-late mouse embryogenesis. Expression is also observed in several adult tissues with highest expression in heart, brain, and liver. Whole-mount in situ hybridization studies reveal apparent ubiquitous expression of ZFEND during mid-gestation stages (embryonic days 11.5, 12.5), while sections of whole-mount embryos reveal much higher expression levels in the neural folds during neural tube closure and at the boundary between the forelimb buds and the body wall. Bioinformatic analysis maps ZFEND to mouse chromosome 8pter, while FLJ10390 resides on 19p13.3-p13.2, a gene-rich region to which a number of disorders have been mapped. More precise mapping indicates that the involvement of FLJ10390 in atherogenic lipoprotein phenotype, familial febrile convulsions 2, and psoriasis susceptibility **cannot** be ruled out.

L3 ANSWER 7 OF 55 MEDLINE
ACCESSION NUMBER: 2002218767 MEDLINE
DOCUMENT NUMBER: 21951688 PubMed ID: 11954993
TITLE: The importance of genetic services for the theory of health: a basis for an integrating view of health.
AUTHOR: Torres Juan Manuel
CORPORATE SOURCE: Centro de Logic y Filosofia de la Ciencia, Universidad Nacional del Sur, Bahia Blanca, Argentina.. jmtorres@criba.edu.ar
SOURCE: MEDICINE, HEALTH CARE, AND PHILOSOPHY, (2002) 5 (1) 43-51. Journal code: 9815900. ISSN: 1386-7423.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Bioethics; Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020417
Last Updated on STN: 20020522
Entered Medline: 20020520

AB The first part of this article shows that our effective means to know and modify directly the human genetic make-up generates singular and difficult situations for the application of fundamental medical categories. Specifically, we demonstrate that in dealing with these situations, some predominant views on health, such as descriptivism or that which reduces the state of health to not having present disabilities, **cannot** provide adequate answers either from the point of view of medical science or in terms of our ordinary intuitions. The second part of the article examines the reasons for the failure of these views to tackle the mentioned situations, proposes solutions to urgent problems and, finally, offers some foundations for an alternative theoretical development, id **est**, for a theory of health able to satisfactorily integrate our genetic dimension.

L3 ANSWER 8 OF 55 MEDLINE
ACCESSION NUMBER: 2001506477 MEDLINE
DOCUMENT NUMBER: 21438260 PubMed ID: 11554468
TITLE: Integrative approaches to determining Csl function.
COMMENT: Comment on: Plant Mol Biol. 2001 Sep;47(1-2):145-60
AUTHOR: Richmond T A; Somerville C R
CORPORATE SOURCE: Carnegie Institution of Washington, Department of Plant Biology, Stanford, CA 94305, USA.. todd@andrew2.stanford.edu
SOURCE: PLANT MOLECULAR BIOLOGY, (2001 Sep) 47 (1-2) 131-43.

Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Commentary
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010917
Last Updated on STN: 20011008
Entered Medline: 20011004

AB While there is an ever-increasing amount of information regarding cellulose synthase catalytic subunits (CesA) and their role in the formation of the cell wall, the remainder of the enzymes that synthesize structural cell wall polysaccharides are unknown. The completion of the Arabidopsis genome and the wealth of the sequence information from other plant genome projects provide a rich resource for determining the identity of these enzymes. Arabidopsis contains six families of genes related to cellulose synthase, the cellulose synthase-like (Csl) genes. Our laboratory is taking a multidisciplinary approach to determine the function of the Csl genes, incorporating genomic, genetic and biochemical data. Information from expressed **sequence tag** (**EST**) projects has revealed the presence of Csl genes in all plant species with a significant number of **ESTs**. Certain Csl families appear to be missing from some species. For example, no examples of CslG **ESTs** have been found in rice or maize. Microarray data and reporter constructs are being used to determine the expression pattern of the CesA and Csl genes in Arabidopsis. Mutations and insertion events have been identified in a majority of the genes in the Arabidopsis CesA superfamily and are being characterized by phenotypic and biochemical analysis. While we **cannot** yet link the function of any of the Csl genes to their respective products, the expression and localization of these genes is consistent with the expected expression pattern of polysaccharide synthases that contribute to the primary cell wall.

L3 ANSWER 9 OF 55 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2002015173 MEDLINE
DOCUMENT NUMBER: 21317932 PubMed ID: 11425220
TITLE: Protein identification based on matrix assisted laser desorption/ionization-post source decay-mass spectrometry.
AUTHOR: Gevaert K; Demol H; Martens L; Hoorelbeke B; Puype M; Goethals M; Van Damme J; De Boeck S; Vandekerckhove J
CORPORATE SOURCE: Flanders Interuniversity, Department of Medical Protein Research, Ghent University, Belgium..
kris.gevaert@rug.ac.be
SOURCE: ELECTROPHORESIS, (2001 May) 22 (9) 1645-51.
Journal code: 8204476. ISSN: 0173-0835.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011204

AB Due to its very short analysis time, its high sensitivity and ease of automation, matrix-assisted laser desorption/ionization (MALDI)-peptide mass fingerprinting has become the preferred method for identifying

proteins of which the sequences are available in databases. However, many protein samples **cannot** be unambiguously identified by exclusively using their peptide mass fingerprints (e.g., protein mixtures, heavily posttranslationally modified proteins and small proteins). In these cases, additional sequence information is needed and one of the obvious choices when working with MALDI-mass spectrometry (MS) is to choose for post source decay (PSD) analysis on selected peptides. This can be performed on the same sample which is used for peptide mass fingerprinting. Although in this type of peptide analysis, fragmentation yields are very low and PSD spectra are often very difficult to interpret manually, we here report upon our five years of experience with the use of PSD spectra for protein identification in sequence (protein or expressed **sequence tag** (**EST**)) databases. The combination of peptide mass fingerprinting and PSD and analysis described here generally leads to unambiguous protein identification in the amount of material range generally encountered in most proteome studies.

L3 ANSWER 10 OF 55 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2001416872 MEDLINE
DOCUMENT NUMBER: 21359029 PubMed ID: 11466257
TITLE: Evaluation of the G protein coupled receptor-75 (GPR75) in age related macular degeneration.
AUTHOR: Sauer C G; White K; Stohr H; Grimm T; Hutchinson A; Bernstein P S; Lewis R A; Simonelli F; Pauleikhoff D; Allikmets R; Weber B H
CORPORATE SOURCE: Institute of Human Genetics, University of Wurzburg, Germany.
SOURCE: BRITISH JOURNAL OF OPHTHALMOLOGY, (2001 Aug) 85 (8) 969-75.
Journal code: 0421041. ISSN: 0007-1161.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200109
ENTRY DATE: Entered STN: 20010910
Last Updated on STN: 20010910
Entered Medline: 20010906

AB BACKGROUND: A long term project was initiated to identify and to characterise genes that are expressed exclusively or preferentially in the retina as candidates for a genetic susceptibility to age related macular degeneration (AMD). A transcript represented by a cluster of five human expressed **sequence tags** (**ESTs**) derived exclusively from retinal cDNA libraries was identified. METHODS: Northern blot and RT-PCR analyses confirmed preferential retinal expression of the gene, which encodes a G protein coupled receptor, GPR75. Following isolation of the full length cDNA and determination of the genomic organisation, the coding sequence of GPR75 was screened for mutations in 535 AMD patients and 252 controls from Germany, the United States, and Italy. Employed methods included single stranded conformational polymorphism (SSCP) analysis, denaturing high performance liquid chromatography (DHPLC), and direct sequencing. RESULTS: Nine different sequence variations were identified in patients and control individuals. Three of these (-30A>C, 150G>A, and 346G>A) likely represent polymorphic variants. Each of six alterations (-4G>A, N78K, P99L, S108T, T135P, and Q234X) were found once in single AMD patients and were considered variants

that could affect the protein function and potentially cause retinal pathology. CONCLUSION: The presence of six potential pathogenic variants in a cohort of 535 AMD patients alone does not provide statistically significant evidence for the association of sequence variation in GPR75 with genetic predisposition to AMD. However, a possible connection between the variants and age related retinal pathology **cannot** be discarded. Functional studies are needed to clarify the role of GPR75 in retinal physiology.

L3 ANSWER 11 OF 55 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2001479475 MEDLINE
DOCUMENT NUMBER: 21414269 PubMed ID: 11522911
TITLE: Identification of Lhcb gene family encoding the light-harvesting chlorophyll-a/b proteins of photosystem II in Chlamydomonas reinhardtii.
AUTHOR: Teramoto H; Ono T; Minagawa J
CORPORATE SOURCE: Laboratory for Photo-Biology, Photodynamics Research Center, The Institute of Physical and Chemical Research (RIKEN), Sendai, 980-0845 Japan.. teramoto@postman.riken.go.jp
SOURCE: PLANT AND CELL PHYSIOLOGY, (2001 Aug) 42 (8) 849-56. Journal code: 9430925. ISSN: 0032-0781.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB051204; GENBANK-AB051205; GENBANK-AB051206; GENBANK-AB051207; GENBANK-AB051208; GENBANK-AB051209; GENBANK-AB051210; GENBANK-AB051211
ENTRY MONTH: 200111
ENTRY DATE: Entered STN: 20010828
Last Updated on STN: 20011105
Entered Medline: 20011101

AB The Lhcb gene family in green plants encodes several light-harvesting Chl a/b-binding (LHC) proteins that collect and transfer light energy to the reaction centers of PSII. We comprehensively characterized the Lhcb gene family in the unicellular green alga, Chlamydomonas reinhardtii, using the expressed **sequence tag** (**EST**) databases. A total of 699 among over 15,000 **ESTs** related to the Lhcb genes were assigned to eight, including four new, genes that we isolated and sequenced here. A sequence comparison revealed that six of the Lhcb genes from C. reinhardtii correspond to the major LHC (LHCII) proteins from higher plants, and that the other two genes (Lhcb4 and Lhcb5) correspond to the minor LHC proteins (CP29 and CP26). No **ESTs** corresponding to another minor LHC protein (CP24) were found. The six LHCII proteins in C. reinhardtii **cannot** be assigned to any of the three types proposed for higher plants (Lhcb1-Lhcb3), but were classified as follows: Type I is encoded by LhcII-1.1, LhcII-1.2 and LhcII-1.3, and Types II, III and IV are encoded by LhcII-2, LhcII-3 and LhcII-4, respectively. These findings suggest that the ancestral LHC protein diverged into LHCII, CP29 and CP26 before, and that LHCII diverged into multiple types after the phylogenetic separation of green algae and higher plants.

L3 ANSWER 12 OF 55 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001206037 MEDLINE
DOCUMENT NUMBER: 21142419 PubMed ID: 11230739
TITLE: Soluble liver antigen: isolation of a 35-kd recombinant

protein (SLA-p35) specifically recognizing sera from patients with autoimmune hepatitis.

AUTHOR: Volkmann M; Martin L; Baurle A; Heid H; Strassburg C P; Trautwein C; Fiehn W; Manns M P

CORPORATE SOURCE: Zentrallabor, Medizinische Klinik und Poliklinik, Universitat Heidelberg, Deutsches Krebsforschungszentrum, Heidelberg, Germany..

Martin_Volkmann@med.uni-heidelberg.de

SOURCE: HEPATOLOGY, (2001 Mar) 33 (3) 591-6.
Journal code: 8302946. ISSN: 0270-9139.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF146396; GENBANK-AJ238617

ENTRY MONTH: 200104

ENTRY DATE: Entered STN: 20010417
Last Updated on STN: 20010417
Entered Medline: 20010412

AB Autoantibodies to soluble liver antigen (SLA) are considered a specific marker of autoimmune hepatitis. We have performed immunoscreening of a human liver gene expression library with an anti-SLA-positive serum. A reactive clone with a 35-kd open reading frame (ORF) and a 563 base pair (bp) 3' untranslated region (UTR) was isolated (soluble liver antigen [SLA]-p35), showing strong homology to an independently isolated putative SLA/liver-pancreas antigen (LP) sequence (Acc. No. AF146396), and a UGA serine tRNA-protein complex (tRNP)((Ser) Sec) related protein (AJ238617), as well as different expression **sequence tag** (**EST**)-clones from lymphatic and oncofetal tissues. Expressed in Escherichia coli, SLA-p35 showed dose-dependent and complete blocking of reactivity to native SLA antigen after preabsorption with the 35-kd recombinant protein. It recognized 67/85 (78.8%) precharacterized anti-SLA-positive sera in dilutions up to 1:40,000 in immunoblot, without detectable cross reactivity in the controls. The commercially available SLA/LP enzymelinked immunosorbent assay (ELISA), by comparison, recognized 63/85 samples (74.1%). Of the negative samples, 18% showed strong inhibition rates (80% and above) in the polyclonal inhibition ELISA. We conlude that the complementary DNA now isolated by 3 independent approaches encodes for the major but not sole antigenic component of soluble liver antigen. Although its truncated form presented here may serve to improve diagnostics based on the new recombinant polypeptide, it currently **cannot** fully replace the polyclonal inhibition ELISA.

L3 ANSWER 13 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:199005 BIOSIS

DOCUMENT NUMBER: PREV200200199005

TITLE: The transcriptome of bone marrow cells in chronic leukemias.

AUTHOR(S): Silva, Wilson A., Jr. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago, Marco A. (1)

CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 550a-551a. http://www.bloodjournal.org/. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11, 2001

ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The complete collection of transcripts generated from the human genome **cannot** be predicted from the genome sequence, but should be directly determined for each tissue, due to variations of gene expression in different tissues and disease states, and because genes can encode multiple transcripts derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million expressed **sequence tags** (**EST**) from different cancer tissues, we constructed a set of cDNAs obtained from bone marrow cells of patients with CML and CLL, that represent partial expressed gene sequences that are biased toward the central coding regions of the resulting transcripts (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000). The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, protein metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative proteins with unknown functions, DNA clones orthologs and paralogs, whereas 852 were classified as no hits. The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in bone marrow cells was compared with other normal and neoplastic tissues from breast, prostate, colon, and brain. Of the 10 larger contigs, 5 genes were commonly expressed in most of the other tissues, one was exclusively found in bone marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in bone marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing protein, beta-globin and Xg antigen. Among 852 contigs that did not match annotated regions of the genome (no hits), the predicted protein sequence of 77 contigs matched known protein domains when evaluated by pfam (protein family database of alignment and HMMs), representing candidate unannoted genes. To search for single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies SMPs by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat Genet 23:452, 1999). A total of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealthy of information provided by this approach demonstrates its usefulness for the analysis of gene expression in specific hematopoietic tissues and diseases.

L3 ANSWER 14 OF 55 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2001161672 MEDLINE
DOCUMENT NUMBER: 21159729 PubMed ID: 11259335
TITLE: The sole gateway to endotoxin response: how LPS was identified as Tlr4, and its role in innate immunity.
AUTHOR: Beutler B; Poltorak A

CORPORATE SOURCE: The Scripps Research Institute, La Jolla, CA 92027, USA.. bruce@scripps.edu
SOURCE: DRUG METABOLISM AND DISPOSITION, (2001 Apr) 29 (4 Pt 2) 474-8.
Journal code: 9421550. ISSN: 0090-9556.
PUB. COUNTRY: United States
Conference; Conference Article; (CONGRESSES)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010618
Last Updated on STN: 20010618
Entered Medline: 20010614

AB Tlr4 has emerged as a specific conduit for the bacterial lipopolysaccharide (LPS) response. The fact that such a protein exists, and furthermore, the fact that it is one member of a family of proteins expressed by mononuclear cells, yields considerable insight into the mechanism by which phagocytes "see" the microbial universe. It **cannot** yet be assumed that all the Tlrs have specificity comparable to that of Tlr4, but it is probable that they do, given the molecular constraints to which all proteins are subject. Indeed, it is remarkable that Tlr4 is able to sense so diverse an array of LPS molecules as it does. The total number of Tlr proteins is not yet known. Although approximately 30 leucine-rich proteins bearing Toll-like cytoplasmic domains might be anticipated based on a survey of the genes in Drosophila, far fewer Toll-like genes have been found in mammals to date, although approximately 2 million expressed **sequence tag** sequences are now archived, and much of the genome has been covered. Some of the Toll-like proteins are, in fact, cytokine receptors. Ten leucine-rich Tlrs have been reported so far. Even a small number of receptors might be sufficient to confer recognition of most pathogens, be they fungi, bacteria, or protozoa. Some such receptors may also play developmental roles. The mutational deletion of Tlr genes alone and in combination with one another may help to establish the functions of each member of this newly emergent family of proteins.

L3 ANSWER 15 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:487312 BIOSIS
DOCUMENT NUMBER: PREV200100487312
TITLE: Subtractive cDNA analysis of spinal cord gene expression following partial sciatic nerve injury (PSNL.
AUTHOR(S): Coyle, D. E. (1)
CORPORATE SOURCE: (1) Department of Anesthesia, Univ Cincinnati, Cincinnati, OH USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 142. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Chronic allodynia develops slowly (days to weeks) following peripheral nerve injury and **cannot** be satisfactory explained without taking into account central mechanisms. This suggests that chronic allodynia requires a cascade of posttranslational and transcriptional events to occur before its development. In order to understand the molecular basis for the development of chronic allodynia this study has used the

subtractive cDNA cloning method to isolate genes that are differentially expressed in the spinal cord following partial sciatic nerve ligation (PSNL). Three "full length" cDNA libraries were generated (normal female, PSNL 7-14, and 15-21 days post-injury). The normal female spinal cord cDNA library (driver) was subtracted from both PSNL spinal cord cDNA libraries (target) by the method of Lin and Sargan (NeuroReport 6, 1981-1984 (1995)). The remaining clones that contained inserts were further screened by hybridization with Cy5-labeled cDNA probes generated from the driver cDNA library (fluorescent Southern Analysis). Of the clones that did not hybridize, the 25% displaying the lowest fluorescent intensity were sequenced (UC DNA Core Facility) and nucleic acid homology searches were performed using the BLAST program. Thirty-six distinct clones were identified and isolated of which 20 (56%) were known genes, 5 (14%) were unknown genes with **EST** matches, and 11 (30%) were novel genes. All genes were verified using RT-PCR using primers based on cDNA sequences and/or by virtual northern analysis. The identified clones indicate that both neurons and glia are involved in the process of change within the spinal cord following PSNL.

L3 ANSWER 16 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151895 BIOSIS
DOCUMENT NUMBER: PREV200200151895
TITLE: The transcriptome of bone marrow cells in chronic leukemia.
AUTHOR(S): Silva-Junior, Wilson A. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago, Marco A.
CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 131b. http://www.bloodjournal.org/. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The complete collection of transcripts generated from the human genome **cannot** be predicted from the genome sequence, but should be directly determined for each tissue, due to variations of gene expression in different tissues and disease states, and because genes can encode multiple transcripts derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million expressed **sequence tags** (**EST**) from different cancer tissues, we constructed a set of cDNAs obtained from bone marrow cells of patients with CML and CLL, that represent partial expressed gene sequences that are biased toward the central coding regions of the resulting transcripts (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000), The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, protein

metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative proteins with unknown functions, DNA clones, orthologs and paralogs, whereas 852 were classified as no hits. The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in bone marrow cells was compared with other normal and neoplastic tissues from breast, prostate, colon, and brain. Of the 10 larger contigs, 5 genes were commonly expressed in most of the other tissues, one was exclusively found in bone marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in bone marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing protein, beta-globin and Xg antigen. Among 852 contigs that did not match annotated regions of the genome (no hits), the predicted protein sequence of 77 contigs matched known protein domains when evaluated by pfam (protein family database of alignment and HMMs), representing candidate unannoted genes. To search for single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies SNPs by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat Genet 23:452, 1999). A total of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealthy of information provided by this approach demonstrates its usefulness for the analysis of gene expression in specific hematopoietic tissues and diseases.

L3 ANSWER 17 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:473332 BIOSIS
DOCUMENT NUMBER: PREV200100473332
TITLE: Integrative approaches to determining Csl function.
AUTHOR(S): Richmond, Todd A. (1); Somerville, Chris R.
CORPORATE SOURCE: (1) Department of Plant Biology, Carnegie Institution of Washington, 260 Panama Street, Stanford, CA, 94305: todd@andrew2.stanford.edu USA
SOURCE: Plant Molecular Biology, (September, 2001) Vol. 47, No. 1-2, pp. 131-143. print.
ISSN: 0167-4412.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB While there is an ever-increasing amount of information regarding cellulose synthase catalytic subunits (CesA) and their role in the formation of the cell wall, the remainder of the enzymes that synthesize structural cell wall polysaccharides are unknown. The completion of the Arabidopsis genome and the wealth of the sequence information from other plant genome projects provide a rich resource for determining the identity of these enzymes. Arabidopsis contains six families of genes related to cellulose synthase, the cellulose synthase-like (Csl) genes. Our laboratory is taking a multidisciplinary approach to determine the function of the Csl genes, incorporating genomic, genetic and biochemical data. Information from expressed **sequence tag** (**EST**) projects has revealed the presence of Csl genes in all plant species with a significant number of **ESTs**. Certain Csl families

appear to be missing from some species. For example, no examples of Csl G **ESTs** have been found in rice or maize. Microarray data and reporter constructs are being used to determine the expression pattern of the CesA and Csl genes in Arabidopsis. Mutations and insertion events have been identified in a majority of the genes in the Arabidopsis CesA superfamily and are being characterized by phenotypic and biochemical analysis. While we **cannot** yet link the function of any of the Csl genes to their respective products, the expression and localization of these genes is consistent with the expected expression pattern of polysaccharide synthases that contribute to the primary cell wall.

L3 ANSWER 18 OF 55 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2001012518 MEDLINE
DOCUMENT NUMBER: 20408867 PubMed ID: 10951213
TITLE: The light-harvesting antenna of brown algae: highly homologous proteins encoded by a multigene family.
AUTHOR: De Martino A; Douady D; Quinet-Szely M; Rousseau B; Crepineau F; Apt K; Caron L
CORPORATE SOURCE: Ecole Normale Superieure, CNRS UMR 8543, Paris, France.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2000 Sep) 267 (17) 5540-9.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001031

AB Accessory light-harvesting complexes (LHCFs) were isolated from the brown alga Laminaria saccharina. Complexes specifically associated with photosystem I or II are identical with each other with respect to molecular mass, isoelectric point and behavior on anion-exchange chromatography or non-denaturing isoelectric focusing. The purified complexes also have similar pigment composition and spectroscopic properties. It is concluded that LHC antennae associated with photosystem I or II **cannot** be distinguished biochemically. After screening of genomic and cDNA libraries produced from L. saccharina sporophytes, six lhcf genes were isolated. Sequence analysis of these lhcf genes showed a high level of homology between the encoded polypeptides. Comparisons with coding sequences of lhcf genes from Macrocystis pyrifera and expressed **sequence tags** from Laminaria digitata (two other Laminariales) indicated that these proteins are probably very similar in all brown algae. Another feature common to the lhcf genes characterized was the presence of an intron in the coding region corresponding to the plastid-targeting presequence. The sequence similarity extended to the 5' and 3' UTRs of several genes. In spite of the common origin of the chloroplasts, no light-regulating elements involved in the expression of the genes encoding the higher-plant light-harvesting proteins has been found in the UTRs.

L3 ANSWER 19 OF 55 MEDLINE
ACCESSION NUMBER: 2001418683 MEDLINE
DOCUMENT NUMBER: 21360614 PubMed ID: 11466977
TITLE: Mining of assembled expressed sequence tag (EST) data for protein families: application to the G protein-coupled receptor superfamily.

AUTHOR: Conklin D; Yee D P; Millar R; Engelbrecht J; Vissing H
CORPORATE SOURCE: MRC Reproductive Biology Unit, Edinburgh.
SOURCE: Brief Bioinform, (2000 Feb) 1 (1) 93-9.
Journal code: 100912837. ISSN: 1467-5463.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

AB The availability of large expressed **sequence tag** (**EST**) databases has led to a revolution in the way new genes are identified. Mining of these databases using known protein sequences as queries is a powerful technique for discovering orthologous and paralogous genes. The scientist is often confronted, however, by an enormous amount of search output owing to the inherent redundancy of **EST** data. In addition, high search sensitivity often **cannot** be achieved using only a single member of a protein superfamily as a query. In this paper a technique for addressing both of these issues is described. Assembled **EST** databases are queried with every member of a protein superfamily, the results are integrated and false positives are pruned from the set. The result is a set of assemblies enriched in members of the protein superfamily under consideration. The technique is applied to the G protein-coupled receptor (GPCR) superfamily in the construction of a GPCR Resource. A novel full-length human GPCR identified from the GPCR Resource is presented, illustrating the utility of the method.

L3 ANSWER 20 OF 55 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2001181872 MEDLINE
DOCUMENT NUMBER: 21098445 PubMed ID: 11173827
TITLE: Cell lines from the same cervical carcinoma but with different radiosensitivities exhibit different cDNA microarray patterns of gene expression.
AUTHOR: Achary M P; Jaggernauth W; Gross E; Alfieri A; Klinger H P;
Vikram B
CORPORATE SOURCE: Department of Radiation Oncology, Albert Einstein College of Medicine of Yeshiva University, and Montefiore Medical Center, Bronx, NY, USA.. achary@aecom.yu.edu
SOURCE: CYTOGENETICS AND CELL GENETICS, (2000) 91 (1-4) 39-43.
Journal code: 0367735. ISSN: 0301-0171.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010329

AB Combining chemotherapy with radiotherapy has improved the cure rate among patients with cancers of the cervix. Although one-half to two-thirds of the patients can be cured by radiation alone, such patients **cannot** be identified at present and must therefore suffer the burden of chemotherapy. Our long-range goal is to identify those cervical cancers that are radiosensitive and could be cured by radiotherapy alone. The advent of methods that permit the simultaneous analysis of expression patterns of thousands of genes, make it feasible to attempt to identify

the molecular events related to radiosensitivity and the associated regulatory pathways. We hypothesize that the sensitivity of tumor cells to ionizing radiation (IR) is determined by the level of expression of specific genes that may be identified with the aid of cDNA microarrays. As the first step in testing this hypothesis, we determined the gene expression differences between two cell lines exhibiting different degrees of radiosensitivity. These were derived from the same tumor prior to treatment from a patient with squamous cell carcinoma of the cervix. The mRNA from these cells was subjected to cDNA analysis on a microarray of 5,776 known genes and **ESTs**. The expression of 52 genes of the total of 5,776 was elevated (maximum 4.1 fold) in the radioresistant cells as compared to the radiosensitive cells. Ten of the 52 sequences are known genes while 42 are **ESTs**. Conversely, the expression of 18 genes was elevated in the sensitive cells as compared to the resistant cells. Seven of these 18 are known genes while eleven are **ESTs**. Among the genes expressed differentially between the resistant and sensitive cells were several known to be associated with response to IR and many more genes and **ESTs** that had not previously been reported to be related to radiosensitivity. The genes that showed the greatest overexpression in the radioresistant cell line were metal-regulatory transcription factor-1, cytochrome P450 CYP1B1, adenomatosis polyposis coli, translation elongation factor-1, cytochrome-c oxidase, whereas in the sensitive cell line, transcription factor NF-kappa-B, metalloproteinase inhibitor-1 precursor, superoxide dismutase-2, insulin-like growth factor binding protein-3, guanine nucleotide-binding protein and transforming growth factor beta-induced protein were overexpressed.

L3 ANSWER 21 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:223870 BIOSIS
DOCUMENT NUMBER: PREV200200223870
TITLE: Cloning and nephron localization of a rabbit kidney KCl cotransporter, KCC4.
AUTHOR(S): Velazquez, Heino (1); Silva, Teresa C.; Andujar, Eleanor
CORPORATE SOURCE: (1) Research, VA Connecticut Healthcare System and Yale University, New Haven, CT USA
SOURCE: Journal of the American Society of Nephrology, (September, 2000) Vol. 11, No. Program and Abstract Issue, pp. 38A. http://www.jasn.org/. print.
Meeting Info.: 33rd Annual Meeting of the American Society of Nephrology and the 2000 Renal Week Toronto, Ontario, Canada October 10-16, 2000
ISSN: 1046-6673.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB We have demonstrated previously chloride-dependent K secretion in renal distal tubules (AJP 242:F46, 1982; AJP 262:F1076, 1992) and postulated the presence of a K-Cl cotransporter in the apical membrane. The recent cloning of K-Cl cotransporter genes (KCC1, KCC2) provides a new approach to the investigation of chloride-dependent K secretion by the renal distal tubule. We attempted to identify a candidate for a novel secretory KCl cotransporter in distal cells by screening expressed **sequence tag** (**EST**) databases for clones homologous to KCC1. KCC1

appears to be expressed in all nephron segments and is not restricted to the distal tubule. Two human **ESTs** with high homology to KCC1 and KCC2 were identified. Rabbit and human cDNA libraries were screened and a partial cDNA clone isolated. The full length rabbit sequence was obtained by PCR and 3' and 5' RACE and is the rabbit homologue to the recently cloned KCC4 isoform in mouse and human. Rabbit KCC4 is 1106 amino acids long and approx. 67, 68, and 65% percent similar to KCC1, KCC2 and KCC3, respectively. A second 5' RACE clone that encodes a truncated protein (1014 amino acids) was identified. Rabbit KCC4 is 84.6% and 87.3% similar to the human and mouse KCC4 sequences with the greatest divergence in the N-terminus. Single-nephron RT/PCR experiments were performed using dissected rabbit tubules and two separate sets of primers (mid-gene; 3' end). In each PCR, agarose gel electrophoresis showed a band of expected size in all nephron segments tested: proximal tubule, thick ascending limb, distal convoluted tubule, connecting tubule, cortical collecting duct, medullary collecting duct and glomerulus. Attempts at single-nephron RT/PCR analysis using unique 5' primers designed to distinguish between KCC4 and the truncated form were inconclusive. We conclude: 1) we cloned the rabbit K-C1-cotransporter homologue to KCC4; 2) KCC4 mRNA expression is detected in all nephron segments of the rabbit; 3) a single cell type may express more than one K-C1 cotransporter isoform; 4) the role of KCC1-4 in renal distal K secretion **cannot** yet be established; 5) recent localization of KCC4 to the basolateral membrane of mouse nephron (FASEB J. 14:A341, 2000) suggests that KCC4 may not be involved in distal tubule apical secretory K flux.

L3 ANSWER 22 OF 55 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 2001060892 MEDLINE
DOCUMENT NUMBER: 20485590 PubMed ID: 11029751
TITLE: Differential gene expression of rat neonatal heart analyzed by suppression subtractive hybridization and expressed sequence tag sequencing.
AUTHOR: Chim S S; Cheung S S; Tsui S K
CORPORATE SOURCE: Department of Biochemistry, The Chinese University of Hong Kong, Shatin, N.T., Hong Kong, China.
SOURCE: JOURNAL OF CELLULAR BIOCHEMISTRY, (2000 Sep 18) 80 (1) 24-36.
Journal code: 8205768. ISSN: 0730-2312.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001222

AB Heart diseases have been one of the major killers among the human population worldwide. Because the vast majority of cardiomyocytes **cannot** regenerate once they cease to proliferate shortly after birth, functionally significant myocardial regeneration is not observed clinically. Whether these cells are terminally differentiated and permanently withdrawn from the cell cycle is controversial, but broadening our understanding of the rapid switch from hyperplastic to hypertrophic growth of cardiomyocytes during neonatal myocardial development may shed light on novel cardiovascular therapies. By suppression subtractive hybridization (SSH) and expressed **sequence tag** (**EST**) sequencing, we analyzed the differential gene expression of rat neonatal heart. SSH yielded subtracted and normalized cDNA libraries

and enhanced the probability of detecting **ESTs**, which represent genes pertinent to signal transduction/cell regulation and replication/transcription/translation machinery, as compared to the traditional **EST** sequencing of heart cDNA libraries.

L3 ANSWER 23 OF 55 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 1999235549 MEDLINE
DOCUMENT NUMBER: 99235549 PubMed ID: 10220143
TITLE: Low yield of polymorphisms from EST blast searching: analysis of genes related to oxidative stress and verification of the P197L polymorphism in GPX1.
AUTHOR: Forsberg L; de Faire U; Morgenstern R
CORPORATE SOURCE: Division of Biochemical Toxicology, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden.. lena.ekstrom@imm.ki.se
SOURCE: HUMAN MUTATION, (1999) 13 (4) 294-300.
Journal code: 9215429. ISSN: 1059-7794.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990618
Last Updated on STN: 19990618
Entered Medline: 19990610

AB To determine new polymorphisms in the antioxidant enzymes superoxide dismutase, glutathione peroxidases, catalase, and microsomal glutathione transferase 1, a search of the human expressed **sequence tags** (**EST**) database was performed (with BLAST 2.0). When any mutation, indicated by the BLAST search, gave rise to a nonconservative amino acid change we performed polymerase chain reaction (PCR) restriction analysis and/or sequence analysis of genomic DNA from human subjects in order to verify these potential polymorphisms. Of nine indicated polymorphisms from the **EST** analysis found in four different antioxidant enzymes, we could verify one, an amino acid substitution Pro-Leu at amino acid position 197 (P197L), in the glutathione peroxidase 1 gene. The corresponding allele frequencies were approximately 70/30%. In addition, a silent mutation (1167T/C) in the catalase gene indicated by the BLAST search could also be verified. Six to nine individuals were analyzed per indicated polymorphism, so that only common polymorphisms would be found. The indicated mutations not verified by direct analysis thus **cannot** be excluded as allelic variation in the human population. These results show that the **EST** database can be used to search for polymorphisms in genes with high abundance in the human **EST** database. In addition to the **EST** analysis, PCR/single-strand conformation polymorphism (SSCP) was employed for the analysis of the microsomal glutathione transferase 1 gene. No polymorphism in the coding sequence could be detected in the gene by either method. The high degree of conservation of the microsomal glutathione transferase 1 gene indicates an important physiological function for this enzyme.

L3 ANSWER 24 OF 55 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 2000018177 MEDLINE
DOCUMENT NUMBER: 20018177 PubMed ID: 10548727
TITLE: Analysis of NotI linking clones isolated from human chromosome 3 specific libraries.
AUTHOR: Kashuba V I; Gizatullin R Z; Protopopov A I; Li J;

Vorobieva N V; Fedorova L; Zabarovska V I; Muravenko O V; Kost-Alimova M; Domninsky D A; Kiss C; Allikmets R; Zakharyev V M; Braga E A; Sumegi J; Lerman M; Wahlestedt C;
Zelenin A V; Sheer D; Winberg G; Grafodatsky A; Kisselev L L; Klein G; Zabarovsky E R

CORPORATE SOURCE: Microbiology and Tumor Biology Center, Karolinska Institute, Stockholm, Sweden.. vlakas@ki.se

SOURCE: GENE, (1999 Nov 1) 239 (2) 259-71.
Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199912

ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991209

AB We have partially sequenced more than 1000 NotI linking clones isolated from human chromosome 3-specific libraries. Of these clones, 152 were unique chromosome 3-specific clones. The clones were precisely mapped using a combination of fluorescence in situ hybridization (FISH) and hybridization to somatic cell or radiation hybrids. Two- and three-color FISH was used to order the clones that mapped to the same chromosomal region, and in some cases, chromosome jumping was used to resolve ambiguous mapping. When this NotI restriction map was compared with the yeast artificial chromosome (YAC) based chromosome 3 map, significant differences in several chromosome 3 regions were observed. A search of the EMBL nucleotide database with these sequences revealed homologies (90-100%) to more than 100 different genes or expressed **sequence tags** (**ESTs**). Many of these homologies were used to map new genes to chromosome 3. These results suggest that sequencing NotI linking clones, and sequencing CpG islands in general, may complement the **EST** project and aid in the discovery of all human genes by sequencing random cDNAs. This method may also yield information that **cannot** be obtained by the **EST** project alone; namely, the identification of the 5' ends of genes, including potential promoter/enhancer regions and other regulatory sequences

L3 ANSWER 25 OF 55 MEDLINE DUPLICATE 14

ACCESSION NUMBER: 1999395631 MEDLINE

DOCUMENT NUMBER: 99395631 PubMed ID: 10466137

TITLE: The importance of reverse genetics in determining gene function in apicomplexan parasites.

AUTHOR: Soete M; Hettman C; Soldati D

CORPORATE SOURCE: ZMBH Zentrum fur Molekulare Biologie Heidelberg, Germany.

SOURCE: PARASITOLOGY, (1999) 118 Suppl S53-61. Ref: 60
Journal code: 0401121. ISSN: 0031-1820.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199909

ENTRY DATE: Entered STN: 19991012
Last Updated on STN: 19991012
Entered Medline: 19990930

AB The phylum Apixomplexa includes obligate intracellular parasites that are of enormous medical and veterinary significance, as they are responsible

for a wide variety of diseases including malaria, toxoplasmosis, coccidiosis, cryptosporidiosis, theileriosis and babesiosis. The **EST** sequencing projects in Toxoplasma gondii and the Plasmodium falciparum genome sequencing project have greatly accelerated gene discovery, revealing for example novel coding sequences restricted to the Apicomplexa. However, easy acquisition of sequence is almost useless if the function of any given gene **cannot** be tested. The establishment of transfection systems in Toxoplasma gondii, Neospora and in several Plasmodium species has provided us with the reverse genetics methods appropriate to the functional analysis of genes. Over the past few years, the discovery of novel genes coupled to the ability to introduce or modify genes has already contributed to a better understanding of cell biology and pathogenesis of these obligate intracellular parasites. Some insights into the complex processes of parasite invasion, differentiation, regulation of gene expression and protein trafficking are emerging although identification of the exact functional roles for many molecules is still awaiting more investigation. This review summarizes progress in this area. It also emphasises the tight link and synergy between Toxoplasma and malaria research. The use of reverse genetics does not guarantee the answer to gene function, so we can learn from both failed and successful experiments about how better and more efficiently to use 'genomics' to accelerate discoveries relevant to the understanding of parasitism by Apicomplexa.

L3 ANSWER 26 OF 55 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 1999231754 MEDLINE
DOCUMENT NUMBER: 99231754 PubMed ID: 10217402
TITLE: Novel BNIP1 variants and their interaction with BCL2 family members.
AUTHOR: Zhang H; Heim J; Meyhack B
CORPORATE SOURCE: Novartis Pharma AG, Oncology, Molecular Genetics, Basel, Switzerland.. hzhang@uhbs.ch
SOURCE: FEBS LETTERS, (1999 Apr 1) 448 (1) 23-7.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF083078; GENBANK-AF083956; GENBANK-AF083957
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990614
Last Updated on STN: 19990614
Entered Medline: 19990601

AB By PCR and **EST** database searches we have identified three novel BNIP1 splice variants, and found that one of them, BNIP1-b, contains a highly conserved BH3 domain. The BNIP1 gene has been assigned to chromosome 5q33-34. Using in vitro protein-protein interaction assays, all BNIP1 variants were shown to interact with BCL2 and also with BCL2L1 (previously Bcl-xL). These interactions are BH3-independent. Furthermore, the BNIP1 variants **cannot** interact with BAX. The results suggest that the BNIP1 variants are novel members of the BCL2 family but function through a mechanism different from other BH3-only members.

L3 ANSWER 27 OF 55 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 1998369652 MEDLINE
DOCUMENT NUMBER: 98369652 PubMed ID: 9704029

TITLE: Cloning and tissue distribution of two new potassium channel alpha-subunits from rat brain.
AUTHOR: Stocker M; Kerschensteiner D
CORPORATE SOURCE: Max-Planck Institut fur Experimentelle Medizin, Gottingen, Germany.. stocker@mail.mpiem.gwdg.de
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998 Jul 30) 248 (3) 927-34.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y17606; GENBANK-Y17607
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19980917
Last Updated on STN: 20000303
Entered Medline: 19980908

AB The expressed **sequence tag** (**EST**) database is a valuable tool to identify functionally related clones, when sequence similarity is so low that standard library screening methods **cannot** be successfully applied. Comparing conserved protein sequences of cloned voltage-gated potassium channels led to the identification and cloning of a new putative potassium channel alpha-subunit from rat brain, Kv9.1. A homologue of this alpha-subunit was also found in human brain tissue. A second alpha-subunit, Kv9.3, most probably belonging to the same subfamily, was also isolated and sequenced.

Tissue distribution and analysis of genomic DNA were performed for both channels. rKv9.1 is expressed exclusively in the central nervous system, whereas rKv9.3 shows a widespread tissue distribution. No currents could be measured in X. oocytes upon injection of rKv9.1 or rKv9.3 cRNA.

L3 ANSWER 28 OF 55 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 1998263247 MEDLINE
DOCUMENT NUMBER: 98263247 PubMed ID: 9600841
TITLE: Protein identification with N and C-terminal sequence tags in proteome projects.
AUTHOR: Wilkins M R; Gasteiger E; Tonella L; Ou K; Tyler M; Sanchez J C; Gooley A A; Walsh B J; Bairoch A; Appel R D; Williams K L; Hochstrasser D F
CORPORATE SOURCE: Central Clinical Chemistry Laboratory, Geneva University Hospital, 24 Rue Micheli-du-Crest, Geneva 14, 1211, Switzerland.
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1998 May 8) 278 (3) 599-608.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980625
Last Updated on STN: 20000303
Entered Medline: 19980616

AB Genome sequences are available for increasing numbers of organisms. The proteomes (protein complement expressed by the genome) of many such organisms are being studied with two-dimensional (2D) gel electrophoresis.

Here we have investigated the application of short N-terminal and

C-terminal **sequence tags** to the identification of proteins separated on 2D gels. The theoretical N and C termini of 15, 519 proteins, representing all SWISS-PROT entries for the organisms Mycoplasma genitalium, Bacillus subtilis, Escherichia coli, Saccharomyces cerevisiae and human, were analysed. **Sequence tags** were found to be surprisingly specific, with N-terminal tags of four amino acid residues found to be unique for between 43% and 83% of proteins, and C-terminal tags of four amino acid residues unique for between 74% and 97% of proteins, depending on the species studied. **Sequence tags** of five amino acid residues were found to be even more specific. To utilise this specificity of **sequence tags** for protein identification, we created a world-wide web-accessible protein identification program, TagIdent (http://www.expasy.ch/www/tools.html), which matches **sequence tags** of up to six amino acid residues as well as estimated protein pI and mass against proteins in the SWISS-PROT database. We demonstrate the utility of this identification approach with **sequence tags** generated from 91 different E. coli proteins purified by 2D gel electrophoresis. Fifty-one proteins were unambiguously identified by virtue of their **sequence tags** and estimated pI and mass, and a further 11 proteins identified when **sequence tags** were combined with protein amino acid composition data. We conlcude that the TagIdent identification approach is best suited to the identification of proteins from prokaryotes whose complete genome sequences are available. The approach is less well suited to proteins from eukaryotes, as many eukaryotic proteins are not amenable to sequencing via Edman degradation, and tag protein identification **cannot** be unambiguous unless an organism's complete sequence is available.

L3 ANSWER 29 OF 55 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 97332671 MEDLINE
DOCUMENT NUMBER: 97332671 PubMed ID: 9188482
TITLE: Differential extraction and protein sequencing reveals major differences in patterns of primary cell wall proteins from plants.
AUTHOR: Robertson D; Mitchell G P; Gilroy J S; Gerrish C; Bolwell G P; Slabas A R
CORPORATE SOURCE: Department of Biological Sciences, Durham University, South Road, Durham DH1 3LE, United Kingdom.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1997 Jun 20) 272 (25) 15841-8.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199707
ENTRY DATE: Entered STN: 19970805
Last Updated on STN: 19970805
Entered Medline: 19970721

AB The proteins of the primary cell walls of suspension cultured cells of five plant species, Arabidopsis, carrot, French bean, tomato, and tobacco, have been compared. The approach that has been adopted is differential

extraction followed by SDS-polyacrylamide gel electrophoresis (PAGE), rather than two-dimensional gel analysis, to facilitate protein sequencing. Whole cells were washed sequentially with the following aqueous solutions, CaCl2, CDTA (cyclohexane diaminotetraacetic acid, DTT (dithiothreitol), NaCl, and borate. SDS-PAGE analysis showed consistent differences between species. From the 233 proteins that were selected for sequencing, 63% gave N-terminal data. This analysis shows that (i) patterns of proteins revealed by SDS-PAGE are strikingly different for all five species, (ii) a large number of these proteins **cannot** be identified by data base searches indicating that a significant proportion of wall proteins have not been previously described, (iii) the major proteins that can be identified belong to very different classes of proteins, (iv) the majority of proteins found in the extracellular growth media are absent from their respective cell wall extracts, and (v) the results of the extraction process are indicative of higher order structure. It appears that aspects of speciation reside in the complement of extracellular wall proteins. The data represent a protein resource for cell wall studies complementary to **EST** (expressed **sequence tag**) and DNA sequencing strategies.

L3 ANSWER 30 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1997:401008 BIOSIS
DOCUMENT NUMBER: PREV199799700211
TITLE: Estimating total body residues and baseline toxicity of complex organic mixtures in effluents and surface waters.
AUTHOR(S): Van Loon, Willem M. G. M.; Verwoerd, Marcel E.; Wijnker, Femke G.; Van Leeuwen, Cees J.; Van Duyn, Piet; Van Deguchte, Cees; Hermens, Joop L. M. (1)
CORPORATE SOURCE: (1) Research Inst. Toxicol., Utrecht Univ., P.O. Box 80176, 3508 TD, Utrecht Netherlands
SOURCE: Environmental Toxicology and Chemistry, (1997) Vol. 16, No. 7, pp. 1358-1365.
ISSN: 0730-7268.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Recently, a new procedure was developed to estimate total body residues (TBRS) in biota after exposure to complex mixtures of organic chemicals in water. The procedure is based on a simulation of bioconcentration using a hydrophobic phase and on the measurement of total molar concentrations on this hydrophobic phase via vapor pressure osmometry and gas chromatography-mass spectrometry. In this paper, the results of the application of this procedure to effluents and surface water are presented. Estimated TBRs (TBR-**ests**) give information on the potential total bioaccumulation of complex mixtures. Moreover, using these estimated total body burdens, baseline toxicity effects can be predicted, including the contributions of chemicals with specific modes of action to the overall baseline toxicity. The advantage of the parameter TBR-**est** is that it determines total molar concentrations of organic chemicals, including those chemicals that are usually not measured because they **cannot** be identified or because their concentrations are below the detection limits of individual compounds.

L3 ANSWER 31 OF 55 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 97368135 MEDLINE
DOCUMENT NUMBER: 97368135 PubMed ID: 9224902

TITLE: Identification of a new member (ZNF183) of the Ring finger gene family in Xq24-25.
AUTHOR: Frattini A; Faranda S; Bagnasco L; Patrosso C; Nulli P; Zucchi I; Vezzoni P
CORPORATE SOURCE: Istituto di Tecnologie Biomediche Avanzate, Consiglio Nazionale delle Ricerche, Milan, Italy.. frattini@itba.mi.cnr.it
SOURCE: GENE, (1997 Jun 19) 192 (2) 291-8.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U08997; GENBANK-U20618; GENBANK-X63222; GENBANK-X81900; GENBANK-X98253; GENBANK-Y07707; GENBANK-Y07708; PIR-S53400
ENTRY MONTH: 199708
ENTRY DATE: Entered STN: 19970825
Last Updated on STN: 20000303
Entered Medline: 19970808

AB Four genes were mapped to the Xq24-25 region by searching the **EST** and the non-redundant database with short tracts of genomic sequences. These were random STSs present in the STS database or sequences derived from CpG islands (EagI-based STSs). One of the four matches corresponded to the full length transcript from the intronless glutamate dehydrogenase gene. The second was the human homolog of the bovine NADH ubiquinone oxidoreductase MWFE subunit gene (GDB symbol: NDUFA1). The other two, ZNF183 and ITBA4, were novel genes whose function **cannot** directly be inferred from their sequence analysis. However, a known motif, the C3HC4 Ring finger domain, shared by various tumor suppressors, DNA repair genes and cytokine receptor-associated molecules, is present at the C terminus of the ubiquitously expressed ZNF183 gene. ITBA4 is expressed at various levels in different tissues and is alternatively processed in brain. Similarity search did not detect any significant match in databases. These results, together with others previously reported by our laboratory, suggest that comparison of genomic and transcribed sequences which are continuously accumulating in databases, can provide 'virtual' mapping of a substantial number of **ESTs** to the specific genomic region which the STSs have been derived from.

L3 ANSWER 32 OF 55 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 97186437 MEDLINE
DOCUMENT NUMBER: 97186437 PubMed ID: 9034012
TITLE: Novel transcribed sequences neighbouring a translocation breakpoint associated with schizophrenia.
AUTHOR: Devon R S; Evans K L; Maule J C; Christie S; Anderson S; Brown J; Shibasaki Y; Porteous D J; Brookes A J
CORPORATE SOURCE: MRC Human Genetics Unit, Western General Hospital, Edinburgh, United Kingdom.
SOURCE: AMERICAN JOURNAL OF MEDICAL GENETICS, (1997 Feb 21) 74 (1) 82-90.
Journal code: 7708900. ISSN: 0148-7299.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-UNKNOWN; SWISSPROT-UNKNOWN
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970507

Last Updated on STN: 19970507
Entered Medline: 19970430

AB A 1.3Mb chromosome 11-specific yeast artificial chromosome (YAC) that spans a t(1;11) translocation breakpoint associated with major psychosis has been used to enrich cDNAs that are encoded within it and expressed in the human foetal brain. Database analysis of the selected fragments led to the identification of 54 clones matching alpha-tubulin, 4 fragments matching two anonymous human expressed **sequence tags** (**ESTs**) and 8 fragments giving no database matches. The clones matching alpha-tubulin led to the identification of a novel alpha-tubulin locus located approximately 250 kb proximal to the translocation breakpoint. Extensive sequence and expression analysis of this locus suggests that this is a processed pseudogene, although a long open reading frame is maintained and the possibility that an abnormally acting protein may be expressed in a highly tissue or developmental specific manner **cannot** be discounted. The novel cDNA fragments map up to 700 kb proximal to the translocation breakpoint and are associated with potential CpG islands. Reverse transcriptase polymerase chain reaction (RT-PCR) expression analysis and high resolution genomic mapping suggest that they may comprise up to three novel genes. No major disruption of the identified fragments could be detected in the genomic DNA of translocation carriers. The psychosis associated with this translocation may therefore be due to position effects on the transcription of these genes or an involvement of translocated chromosome 1 sequences.

L3 ANSWER 33 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1995:28067 BIOSIS
DOCUMENT NUMBER: PREV199598042367
TITLE: Inaccuracy of noninvasive estimates of VD/VT in clinical exercise testing.
AUTHOR(S): Lewis, David A.; Sietsema, Kathy E.; Casaburi, Richard; Sue, Darryl Y.
CORPORATE SOURCE: Harbor-UCLA Med. Cent., 1000 W. Carson St., Box 405, Torrance, CA 90509 USA
SOURCE: Chest, (1994) Vol. 106, No. 5, pp. 1476-1480. ISSN: 0012-3692.
DOCUMENT TYPE: Article
LANGUAGE: English

AB To evaluate the accuracy of noninvasive estimates of V-D/V-T in clinical exercise testing, we compared measurements of standard V-D/V-T with estimates based either on end-tidal CO-2 (V-D/V-T-ET) or a published estimate of arterial PCO-2 (V-D/V-T-**est**) at peak exercise in 68 patients. Using regression analysis, we identified highly significant differences (p lt 0.001) between each method and V-D/V-T-stand across a broad range of observed V-D/V-T. Assuming a normal exercise V-D/V-T ltoreq 0.30, estimate methods were specific but were insensitive (50 percent for V-D/V-T-ET and 57 percent for V-D/V-T-**est**) for identifying patients with abnormal gas exchange during exercise. Separate analysis of subgroups based on resting pulmonary function did not identify any group for which either method was acceptable. Our analysis showed that errors in estimating PaCO-2, which are amplified by the Bohr equation when calculating V-D/V-T, are responsible for the inaccuracies of each noninvasive method. We conclude that noninvasive estimates of PaCO-2 **cannot** replace measured arterial PCO-2 for calculation of V-D/V-T during exercise.

L3 ANSWER 34 OF 55 MEDLINE
ACCESSION NUMBER: 94376965 MEDLINE
DOCUMENT NUMBER: 94376965 PubMed ID: 8090290
TITLE: [Arterial pressure in obese subjects during ergometric stress test and recovery].
Comportamento della pressione arteriosa in soggetti obesi durante sforzo e nel recupero.
AUTHOR: Irace L; Sarubbi B; Ducceschi V; Lucca P; Spadaro P; Iacono
A
CORPORATE SOURCE: Cattedra di Cardiologia, Facolta di Medicina e Chirurgia, II Universita degli Studi di Napoli.
SOURCE: MINERVA CARDIOANGIOLOGICA, (1994 May) 42 (5) 203-9.
Journal code: 0400725. ISSN: 0026-4725.
PUB. COUNTRY: Italy
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Italian
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199410
ENTRY DATE: Entered STN: 19941031
Last Updated on STN: 19941031
Entered Medline: 19941017

AB In obesity, the systemic resistances (SR) are reduced while the blood volume is increased. The rise of cardiac output (CO), stress-induced, produces an increase in blood pressure (BP), as an hypertensive behavior of the stress-response. The aim of our study is to evaluate if, in obese subjects, the considerable increase of BP is more related to the rise of CO than to the rise of SR. For this reason we studied the behavior of BP through indexes derived from the ratio of SBP values at the 1st, 3rd, 5th, 10th minutes of the recovery by the SBP value at the acme of stress. These indexes are under neurovegetative control, and were shown to be impaired in hypertensive pts. The results of ergometric stress test (**EST**) of 37 obese subjects (Ob+) (27 males and 10 females, mean age 46.2 +/- 7.3 years), determined according to Lorentz's formula, was compared with the parameters deduced from the **EST** of 18 normal subjects (Ob-) (13 males and 5 females, mean age 36.7 +/- 8.5). The exercise showed an increase, more pronounced in Ob+ subjects, of SBP and DBP, and this also persisted in the recovery phase. Although BP was significantly higher in the Ob+group, the SBP indexes did not differ in the two groups. Then, from these data it can be deduced that, although during **EST** in obese subjects there is an absolute increase of BP and this persists in the recovery phase, the behavior of this parameter probably **cannot** be related to alteration of neurovegetative system as demonstrated by the normal SBP indexes.

L3 ANSWER 35 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1993:269804 BIOSIS
DOCUMENT NUMBER: PREV199396000029
TITLE: Differentiation of Lolium perenne L. and Lolium multiflorum
Lam. seed by two esterase isoforms.
AUTHOR(S): Griffith, S. M. (1); Banowetz, G. M.
CORPORATE SOURCE: (1) USDA-ARS, National Forage Seed Production Res. Cent. Corvallis, Oregon 97331 USA
SOURCE: Seed Science and Technology, (1992) Vol. 20, No. 3, pp. 343-348.

ISSN: 0251-0952.
DOCUMENT TYPE: Article
LANGUAGE: English
AB When Lolium perenne L. (perennial ryegrass) seed is contaminated by L. multiflorum Lam. (Italian ryegrass), it **cannot** be marketed as certified seed. It would be useful if a reliable genetic marker could be found that would distinguish between L. multiflorum and L. perenne seed. One potential marker may be an L. multiflorum specific seed esterase, **Est**-1. The objectives of this research were: 1) to examine seeds of 18 L. multiflorum and 74 L. perenne cultivars to determine if **Est**-1 activity is unique to L. multiflorum; and 2) to determine if **Est**-1 activity exists in seeds of other Lolium species. Analyses were performed using both native polyacrylamdie gel electrophoresis (native-PAGE) and isoelectric focusing electrophoresis (IEF-PAGE). Following electrophoresis, gels were stained for esterase activity. Results of this investigation confirmed earlier reports showing the existence of a unique L. multiflorum seed esterase isoenzyme, not present in L. perenne. Through high resolution native-PAGE, a total of two **Est**-1 esterase isoforms (**Est**-1a and **Est**-1b) were identified. These forms were present together in seeds of all L. multiflorum cultivars examined. The pI of both **Est**-1 isoforms was 5.15. An esterase of 5.15 pI was also found in L. remotum Schrank. seed. **Est**-1 activity was not detected in L. canariense Steud., L. persicum Boiss., L. temulentum L., L. rigidum Gaudin., and L. subulatum Vis. It appears that both isoforms could be used as markers to distinguish between L. perenne an L. multiflorum seed.

L3 ANSWER 36 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1991:203413 BIOSIS
DOCUMENT NUMBER: BA91:106638
TITLE: EXPERIMENT TO MEASURE THE EFFECT OF PASTURING FIRE AND CUTTING ON WOOD AND GRASS PRODUCTION IN A TREE SAVANNA OF NORTH CAMEROON.
AUTHOR(S): PELTIER R; EYOG-MATIG O
CORPORATE SOURCE: INGENIEUR RECHERCHES CTFT.
SOURCE: BOIS FOR TROP, (1989 (1991)) 0 (221), 3-23.
CODEN: BFTRAO. ISSN: 0006-579X.
FILE SEGMENT: BA; OLD
LANGUAGE: Spanish
AB To manage natural bush land, Cameroonian foresters have created and have been responsible for protecting national parks and reserves. As a result of very stringent controls, vegetation has regenerated and wildlife has thrived. In areas that were less well protected, game has disappeared and trees have been cleared. Local populations oppose measures, such as strict preservation, that don't provide any tangible benefits. Ecological reserves are costly and **cannot** be expanded. Areas of tree savanna are also suffering. They will soon no longer provide any benefits such as fuelwood, poles, construction, pastures, fiber, traditional medicines... They will no longer be available as sources of natural foods during periods of scarcity. No longer will they be available for controlling surface erosion. Simpler and more conservationist methods were needed to ensure that tree savannas were maintained by farmers and herdsmen. The first experiment of the Nord-**Est** Benoue project at Bibemi was abandoned for lack of funding and was destroyed by fire. In 1985, another experiment to measure the effect of pasturing, fire and cutting on wood and grass production was established at Laf-Badjava by CRF

(Forestry Research Center). This experiment was for demonstration purposes. It was located along a main road and was aimed at decision makers. It showed what forest management is, how to establish firebreaks, how to motivate local participation especially wood cutters and herdsmen. Within this context, the Laf reservoir should result in more water available for the village and should encourage settlement. It is a split-plot experiment with two repetitions and three levels. First level (browsing): protected (x1) or not (x2) from browsing; second level (bushfire): permanent protection (y1) or during two years out of 3 (y2), bushfire every year early (y3) or late (y4) in the dry season; third level (wood harvesting): no wood harvesting (z1), harvesting of all valuable species every 3 years (z2), harvesting with respect to some species and some forest management practices every 6 years (z3). The establishment of grasses in bare places has been monitored. This seeems to be possible if protection against fire and excessive browsing is ensured. Reestablishment can be helped along by lying branches on the soil or by tilling the soil. It is essential to ensure protection against fire in order to protect the stand and to encourage regeneration and improve wood production. Under the following conditions: 800 mm of rainfall and on soils allowing at most 1.5 m3/ha/yr of wood production, the protection of a degraded stand of tree savanna for 3 years resulted in a wood productivity rate of 0.5 m3/ha/yr. Within three years of harvest, the following species: Acacia hockii, Dichrostachys glomerata, Piliostigma reticulum, had grown to their original proportions. Low intensity pasturing helps wood production. Under these conditions, the competitive effect of grasses and the intensity of grass fires is minimized. As a result of the lack of such beneficial practices, the authors hope that this work will stimulate other researchers to examine the results reported here. The authors recommend the socio-economic studies be undertaken to determine if villagers can manage extensive areas of forest. Such studies should be undertaken within the context of general land management studies.

L3 ANSWER 37 OF 55 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 90047670 MEDLINE
DOCUMENT NUMBER: 90047670 PubMed ID: 2813784
TITLE: Myocardial uptake and clearance of T1-201 in healthy subjects: comparison of adenosine-induced hyperemia and exercise stress.
COMMENT: Comment in: Radiology. 1990 Jun;175(3):877
AUTHOR: Siffring P A; Gupta N C; Mohiuddin S M; Esterbrooks D J; Hilleman D E; Cheng S C; Sketch M H Sr; Frick M P
CORPORATE SOURCE: Department of Radiology, Creighton University School of Medicine, Omaha, NE 68131.
SOURCE: RADIOLOGY, (1989 Dec) 173 (3) 769-74.
Journal code: 0401260. ISSN: 0033-8419.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 198912
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19900328
Entered Medline: 19891221

AB Pharmacologic stress testing with dipyridamole is useful in patients undergoing thallium-201 myocardial perfusion scintigraphy who

cannot adequately exercise. Because dipyridamole increases coronary blood flow by reducing the metabolism of adenosine, the authors compared the uptake and clearance of T1-201 following exercise stress testing (**EST**) and resting intravenous infusion of adenosine (AI) in crossover fashion in 20 healthy men. No perfusion defects or areas of redistribution were noted in any of the scans. Mean absolute myocardial T1-201 uptake was 1.3 times greater with AI than with **EST**. Mean absolute extracardiac uptake was 2.0 times greater with AI. Mean T1-201 myocardial clearance was virtually the same in all AI and **EST** views. During AI, 70% of the subjects experienced subjective side effects, mean arterial blood pressure decreased by 15%, and heart rate increased by 48%. The effects of adenosine on T1-201 kinetics in the myocardium are similar to those of **EST**. Adenosine may be useful as a pharmacologic stress agent in patients undergoing T1-201 myocardial perfusion scintigraphy.

L3 ANSWER 38 OF 55 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 89137919 MEDLINE
DOCUMENT NUMBER: 89137919 PubMed ID: 3147215
TITLE: Linkage disequilibrium in natural and experimental populations of Drosophila melanogaster.
AUTHOR: Smit-McBride Z; Moya A; Ayala F J
CORPORATE SOURCE: Department of Ecology and Evolutionary Biology, University of California, Irvine 92717.
SOURCE: GENETICS, (1988 Dec) 120 (4) 1043-51.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198904
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19900306
Entered Medline: 19890404

AB We have studied linkage disequilibrium in Drosophila melanogaster in two samples from a wild population and in four large laboratory populations derived from the wild samples. We have assayed four polymorphic enzyme loci, fairly closely linked in the third chromosome: Sod **Est**-6, Pgm, and Odh. The assay method used allows us to identify the allele associations separately in each of the two homologous chromosomes from each male sampled. We have detected significant linkage disequilibrium between two loci in 16.7% of the cases in the wild samples and in 27.8% of the cases in the experimental populations, considerably more than would be expected by chance alone. We have also found three-locus disequilibria in more instances than would be expected by chance. Some disequilibria present in the wild samples disappear in the experimental populations derived from them, but new ones appear over the generations. The effective population sizes required to generate the observed disequilibria by randomness range from 40 to more than 60,000 individuals in the natural population, depending on which locus pair is considered, and from 100 to more than 60,000 in the experimental populations. These population sizes are unrealistic; the fact that different locus-pairs yield disparate estimates within the same population argues against the likelihood that the disequilibria may have arisen as a consequence of population bottlenecks. Migration, or population mixing, **cannot** be excluded as the process generating the disequilibria in the wild samples, but can

in the experimental populations. We conclude that linkage disequilibrium in these populations is most likely due to natural selection acting on the allozymes, or on loci very tightly linked to them.

L3 ANSWER 39 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:134604 BIOSIS
DOCUMENT NUMBER: BA87:69257
TITLE: ELECTROPHORETIC MARKERS FOR THE WHITEFISH SPECIES PAIR COREGONUS-PALLASI AND COREGONUS-PELED.
AUTHOR(S): KOLJONEN M-L; KOSKINIEMI J; PASANEN P
CORPORATE SOURCE: FINNISH GAME AND FISHERIES RES. INST., FISHERIES DIV., P.O. BOX 202, SF-00151, HELSINKI.
SOURCE: AQUACULTURE, (1988) 74 (3-4), 217-226. CODEN: AQCLAL. ISSN: 0044-8486.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB The paper examines the possibility of differentiating Coregonus pallasi (sensu Svardson, 1979) and Coregonus peled (Gmelin) on the basis of electrophoretic markers. The two species have similar numbers or gill rakers and, in breeding work, young fish and possible hybrids have been especially difficult to identify on the basis of their morphology. Populations of both species and their hybrids were analysed electrophoretically. The examination covered 12 enzyme systems, corresponding to 24 loci. The polymorphic loci were: **Est**-1, Mdh-3,4, Me-3, Me-4, Pgi-1, Pgm-2, Pep-2 and Sod-2. The amount of genetic variation was about the same for the two species (7.5%), and was fairly high compared with that of other salmonids. The genetic identity of the species was 0.854, which is less than for conspecific populations in general, but fairly high for separate species. The species could be differentiated on the basis of two diagnostic isozyme systems: the Pgm-1 locus and the secondary band of the Cpk-1,2 loci. The different alleles were also very nearly fixed at the Sod-2 locus. Hybrids can be separated with certainty from C. peled, but approximately 1% of them **cannot** be differentiated from C. pallasi. The use of electrophoretic markers is discussed.

L3 ANSWER 40 OF 55 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 88176329 MEDLINE
DOCUMENT NUMBER: 88176329 PubMed ID: 3444714
TITLE: Endoscopy in the diagnosis and treatment of benign stenosis of the papilla of Vater.
AUTHOR: Tulassay Z; Papp J; Kollin E
CORPORATE SOURCE: First Department of Medicine, Semmelweis University Medical School, Budapest, Hungary.
SOURCE: ACTA MEDICA HUNGARICA, (1987) 44 (4) 371-5. Journal code: 8400269. ISSN: 0236-5286.
PUB. COUNTRY: Hungary
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198805
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19900308
Entered Medline: 19880502
AB Of 921 endoscopic sphincterotomies (**EST**) performed by the authors, 110 (12%) were done for benign stenosis of papilla of Vater. Based on these data, they consider the possibilities of endoscopic

diagnosis and treatment in the stenosis of papilla. One of the conditions for the diagnosis of papilla stenosis is the detectability of dilated biliary tract by endoscopic retrograde cholangiography. But this **cannot** be taken as a specific sign because, e.g., the biliary tract may become dilated in spite of normal sphincter tone after gall-bladder removal. At the same time, biliary tract dilation is a diagnostic criterion for papilla stenosis, and abnormal findings in biliary scintigraphy and the laboratory syndrome consistent with cholestasis **cannot** be avoided. **EST** is the method of first choice in the treatment of papilla stenosis in comparison to surgery. The complications of **EST**, however, occur in papilla stenosis more frequently than in choledocholithiasis (8.8%). Bleeding and cholangitis are responsible for the excess incidence.

L3 ANSWER 41 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1988:90 BIOSIS
DOCUMENT NUMBER: BA85:90
TITLE: GENETIC VARIABILITY AND SOME PROPERTIES OF SUNFLOWER ESTERASE.
AUTHOR(S): ALEXANDRESCU V; EL-KADOUY S A; EL-SHOUNY F M
CORPORATE SOURCE: I.C.C.P.T., FUNDULEA, BD. MARASTI 61, BUCURESTI, ROMANIA.
SOURCE: REV ROUM BIOCHIM, (1987) 24 (3), 205-210.
CODEN: RRBCAD. ISSN: 0001-4214.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB The biosynthesis of sunflower .alpha.-naphthyl esterase is controlled by two loci (**Est** 1 and **Est** 2). Within 12 inbred lines the locus **Est** 1 is active especially in cotyledons during germination, when 5 alloenzymes were noted, and the locus **Est** 2 is active mainly in the kernels, where 3 alloenzymes are occurring being suitable for use as biochemical markers. The roots and leaves contain the enzyme of both loci which exhibits a low activity and a bad electrophoretical resolution. The analysis of the simple hybrids heterologous for this character, the effects of urea, SDS, 2-mercaptoethanol, temperature of inactivation, and the antigenic character show that the molecule of .alpha.-naphthyl esterase isoenzymes is a monomer, that in some plant organs is bound to some other substances, and that the two isoenzymes are different from the point of view of their physical and chemical properties as well as from the antigenical one. The alloenzymes **cannot** be distinguished from the point of view.

L3 ANSWER 42 OF 55 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 86165790 MEDLINE
DOCUMENT NUMBER: 86165790 PubMed ID: 3957005
TITLE: Temporal and microgeographic variation in allozyme frequencies in a natural population of Drosophila buzzatii.
AUTHOR: Barker J S; East P D; Weir B S
CONTRACT NUMBER: GM 11546 (NIGMS)
SOURCE: GENETICS, (1986 Mar) 112 (3) 577-611.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198604
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19970203
Entered Medline: 19860425
AB Temporal variation in allozyme frequencies at six loci was studied by

making monthly collections over 4 yr in one population of the cactophilic species Drosophila buzzatii. Ten sites were defined within the study locality, and for all temporal samples, separate collections were made at each of these sites. Population structure over microgeographic space and changes in population structure over time were analyzed using F-statistic estimators, and multivariate analyses of allele and genotype frequencies with environmental variables were carried out. Allele frequencies showed significant variation over time, although there were no clear cyclical or seasonal patterns. A biplot analysis of allele frequencies over seasons within years and over years showed clear discrimination among years by alleles at four loci. During the 4 yr, three alleles showed directional changes which were associated with directional changes in environmental variables. Significant associations with one or more environmental variables were found for allele frequencies at every locus and for both expected and observed heterozygosities (except those for **Est**-1 and **Est**-2). Thus, variation in allele frequencies over time **cannot** be attributed solely to drift. Significant linkage disequilibria were detected among three loci (**Est**-2, Hex and Aldox), but there was no evidence for spatial or temporal patterns. The F-statistic analyses showed significant differentiation among months within years for all loci, but the statistic used (coancestry) was heterogeneous among loci. Estimates of F (inbreeding) for all loci were significantly different from zero, with the loci in four groups, Adh-1 (negative), Pgm(small positive), **Est**-2 and Hex (intermediate) and **Est**-1 and Aldox (high positive). The correlation of genes within individuals within populations (f) for each locus in each month by site sample differed among loci, as did the (f) for each locus in each month by site sample differed among loci, as did the patterns of change in f over time (seasons). Heterogeneity in the F-statistic estimates indicates that natural selection is directly or indirectly affecting allele and genotype frequencies at some loci. However, the F-statistic analyses showed essentially no microgeographic structure (i.e., among sites), although there was significant heterogeneity in allele frequencies among flies emerging from individual rots. Thus, microspatial heterogeneity probably is most important at the level of individual rots, and coupled with habitat selection, it could be a major factor promoting diversifying selection and the maintenance of polymorphism.(ABSTRACT TRUNCATED AT 400 WORDS)

L3 ANSWER 43 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1987:125715 BIOSIS
DOCUMENT NUMBER: BA83:64776
TITLE: HETEROZYGOSITY AND DEVELOPMENTAL TIME IN DROSOPHILA-MELANOGASTER.
AUTHOR(S): GIRARD P
CORPORATE SOURCE: UNIV. PARIS 7, LAB. GENET. POPULATIONS U.A. C.N.R.S. 693, TOUR 42-43, 2, PLACE JUSSIEU, F 75005 PARIS.
SOURCE: GENET SEL EVOL, (1986) 18 (3), 261-278.
CODEN: GSEVD8.
FILE SEGMENT: BA; OLD
LANGUAGE: French
AB Individuals extracted from 3 natural populations of Drosophila melanogaster have been used to make strains polymorphic for 1, 2 or 6 loci (Acph, Adh, .alpha.-Gpdh, **Est**-6, **Est**-C, and Pgm). A relation between development time and genotype has been looked for. The results are the following: 1) Development time is highly different from one genotype to another. 2) Heterozygous individuals have a shorter development time than homozygous. 3) The extreme differences are greater

in case of 2 loci segregation than in case of one. 3) The 6 loci segregation demonstrate a significant negative correlation between development time and heterozygosity. 5) Therefore, the large variability in each class of heterozygosity **cannot** be explained only by the number of different genotypes in each class. Our results are in good agreement with a systematic overdominance of heterozygous enzymatic loci, a hypothesis that does not exclude the existence of some deleterious genes.

L3 ANSWER 44 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1986:340363 BIOSIS
DOCUMENT NUMBER: BA82:54567
TITLE: CONTRIBUTION TO THE STUDY OF ESTERASES IN 4 SUBSPECIES OF IDOTEA-BALTHICA.
AUTHOR(S): GILARD J-P; LEGRAND-HAMELIN E
CORPORATE SOURCE: LAB. BIOLOGIE ANIMALE, E.R.A. C.N.R.S., NO. 230, U.E.R. SCI., 86022, POITIERS CEDEX, FRANCE.
SOURCE: BIOCHEM SYST ECOL, (1986) 14 (2), 223-232.
CODEN: BSECBU. ISSN: 0305-1978.
FILE SEGMENT: BA; OLD
LANGUAGE: French
AB In Idotea balthica, .alpha. esterase2 and .beta. esterase3 have been tested against nine substrates and nine inhibitors. They are dependent on two polyallelic independent loci. **Est2** offers alternative alleles in Mediterranean and Nordic populations. The variation in frequency of alleles at locus **Est3** allows one to characterize the subspecies stagnea compared with tricuspidata and balthica but **cannot** be used to separate this subspecies of basteri.

L3 ANSWER 45 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1987:251057 BIOSIS
DOCUMENT NUMBER: BA84:4029
TITLE: ESTERASE-6 POLYMORPHISM IN DROSOPHILA-MELANOGASTER EFFECTS OF TEMPERATURE AND METHYL MALONATE ON GENOTYPIC TRAJECTORIES IN POLYMORPHIC POPULATIONS SET UP WITH HIGHLY INBRED LINES.
AUTHOR(S): COSTA R; ZONTA L; JAYAKAR S D; NIGRO L
CORPORATE SOURCE: DEP. BIOL., UNIV. PADUA, VIA LOREDAN 10, 35100 PADOVA, ITALY.
SOURCE: J GENET, (1986 (RECD 1987)) 65 (3), 175-192.
CODEN: JOGNAU. ISSN: 0022-1333.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB It is generally difficult to identify possible effects of selection at a specific locus because of the heterogeneity of the genetic background. Geographical patterns of **Est**-6 gene frequencies suggest that there is selection at this locus but selection on loci closely linked to it **cannot** be excluded. Differences in catalytic properties between allozymes have been shown in vitro; further, several laboratory studies have shown apparent fitness differences between allozymes. Our study used inbred lines highly homogeneous in the genetic background. Four populations were set up from **Est**-6S and **Est**-6F homozygous females inseminated by males of the same genotype at each combination of three factors: temperature (18 and 25.degree. C); methyl malonate (presence or absence); input gene frequencies [p(S) = 0.2 and 0.8]. The populations were sampled periodically for about 28 generations. Methyl malonate was chosen to exert pressure in the enzymatic function of esterase-6. Statistical analyses show that: there are no sex differences;
gene frequencies changes from input values to those of the first sampling,

when only individuals of the first generation are present at 18.degree. C or individuals of the second generation just begin to appear at 25.degree.
C; gene frequencies do not change thereafter and Hardy-Weinberg equilibrium is established. The changes in gene frequencies observed in the first generations suggest that **Est**-6 can under certain conditions be a target of selection. Such conditions may not, however, occur in natural populations.

L3 ANSWER 46 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1986:223556 BIOSIS
DOCUMENT NUMBER: BA81:114856
TITLE: ACUTE AND CHRONIC ACETAZOLAMIDE ADMINISTRATION IN DBA AND C-57 MICE EFFECTS OF AGE.
AUTHOR(S): ENGSTROM F L; WHITE H S; KEMP J W; WOODBURY D M
CORPORATE SOURCE: DIV. NEUROPHARMACOLOGY AND EPILEPTOLOGY, DEP. PHYSIOLOGY, 410 CHIPETA WAY NO. 167, SALT LAKE CITY, UT 84108, USA.
SOURCE: EPILEPSIA, (1986) 27 (1), 19-26.
CODEN: EPILAK. ISSN: 0013-9580.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB The clinical utility of the carbonic anhydrase (CA) inhibitor acetazolamide (ACTZ) is limited because of rapid development of tolerance to its effects. Tolerance is thought to develop as a result of glial cell proliferation and/or increased CA synthesis. DBA mice, susceptible to audiogenic seizures (AGSs) in an age-dependent manner, have increased CA activity as compared with C57 (non-audiogenic seizure susceptible) mice at
21 and 110 days of age. The present work utilized ACTZ to help determine the relationship between increased CA activity in brain and AGSs in DBA mice. Also, minimal electroshock seizure threshold (**EST**) was measured at various ages in DBA and C57 mice to determine age-related changes in CNS excitability. **EST** was significantly lower in DBA as compared with C57 mice at 18 days and between 40 and 115 days of age, suggesting that DBA mice remain hyperexcitable to electrical stimulation after they develop resistance to AGSs. ACTZ ED50s against maximal electroshock seizures (MES) were significantly higher in DBA as compared with C57 mice at 26, 36, and 115 days of age. This finding correlates with
higher CA activity in this strain at 110 days of age, noted previously. However, at 21 days of age, when CA activity is also higher in DBA versus C57 mice, there were no significant differences in ACTZ ED50s against MES between the strains. ACTZ ED50s against AGSs in DBA mice were considerably
lower than ACTZ ED50s against MES in either strain, suggesting that a particular fraction of CA is intimately involved in the production of AGSs. Chronic administration of ACTZ to both strains of mice at 26 and 114
days of age demonstrated that C57 mice were able to develop tolerance to this drug as demonstrated by increases in CA activity and ED50s. In contrast, DBA mice were not able to develop tolerance, probably because they are already producing CA at a maximal rate and **cannot** further induce synthesis of this enzyme.

L3 ANSWER 47 OF 55 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 85205940 MEDLINE
DOCUMENT NUMBER: 85205940 PubMed ID: 3158585
TITLE: Population genetics of polymorphisms in Cardiff newborn. Relationship between blood group and allozyme heterozygosity and birth weight.
AUTHOR: Ward R D; Sarfarazi M; Azimi-Garakani C; Beardmore J A

SOURCE: HUMAN HEREDITY, (1985) 35 (3) 171-7.
Journal code: 0200525. ISSN: 0001-5652.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198507
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19900320
Entered Medline: 19850718

AB A newborn population of Cardiff, Wales, was screened for variation at three blood group loci (ABO, Rhesus and MN) and four enzyme loci (ACP-1, PGM-1, ADA and **EST**-D). Birth weights were measured. There were no significant differences between mean birth weights or birth weight variances for individuals homozygous or heterozygous at the MN and the four enzyme loci. (ABO and Rhesus loci **cannot** be used in these tests.) There was no significant heterogeneity in contingency tables relating phenotypes at the seven loci to birth weight. There were no significant differences in mean heterozygosity per locus between babies placed in different birth weight categories, ranging from 2.5 to 4.2 kg. The genetic variation screened appears therefore to be neutral with respect to this character.

L3 ANSWER 48 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1985:316248 BIOSIS
DOCUMENT NUMBER: BA79:96244
TITLE: MALATE DEHYDROGENASE AND NON-SPECIFIC ESTERASE ISOENZYMES OF APIS-FLOREA APIS-DORSATA AND APIS-CERANA AS DETECTED BY ISOELECTRIC FOCUSING.
AUTHOR(S): NUNAMAKER R A; WILSON W T; AHMAD R
CORPORATE SOURCE: USDA, ARS, HONEY BEE PESTICIDES/DISEASES RES., UNIVERSITY STATION, BOX 3168, LARAMIE, WYOMING 82071.
SOURCE: J KANS ENTOMOL SOC, (1984 (RECD 1985)) 57 (4), 591-595.
CODEN: JKESA7. ISSN: 0022-8567.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Isoelectric focusing on polyacrylamide gels was used to separate isoenzymes of malate dehydrogenase (MDH) and non-specific esterases (**EST**) of Apis florea F., A. dorsata F., and A. cerana F. At least for certain populations, the **EST** locus can be used to differentiate between these 3 spp. of Apis. The isoenzymes of MDH, on the other hand, **cannot** be used to distinguish A. dorsata from A. cerana. None of the test populations of the 3 spp. examined exhibited intraspecific genetic variability.

L3 ANSWER 49 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1982:300546 BIOSIS
DOCUMENT NUMBER: BA74:73026
TITLE: EFFECT OF LEAF AREA INCIDENT RADIATION AND MOISTURE STRESS ON REFLECTANCE OF NEAR IR RADIATION FROM A CORN ZEA-MAYS CANOPY.
AUTHOR(S): DALE R F; SCHEERINGA K L; HODGES H F; HOUSLEY T L
CORPORATE SOURCE: AGRONOMY DEP., PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907.
SOURCE: AGRON J, (1982) 74 (1), 67-73.
CODEN: AGJOAT. ISSN: 0002-1962.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Research was conducted to monitor continuously incident near IR radiation (IR .dwnarw.) and reflectance (IR .uparw.) from corn (Z. mays L.) and to relate the reflectance ratio (IR .uparw.)/IR .dwnarw.) to green leaf area

index (LAI), IR .dwnarw., and moisture stress indices. The experiment was conducted at West Lafayette, Indiana [USA] on a Typic Argiaquoll (Chalmers silt loam) in 1973 and 1974 and on dune sand in 1975 and 1976. Under non-moisture stress (ns) conditions, LAI was used in a function (FLAI) to identify the ratio of green plant cover (RGPC). Linear regressions showed that as FLAI or RGPC increased from 0 to 1, (IR .uparw./IR .dwnarw.)ns increased an average of 9%. For each cal cm-2 h-1 increase in IR .dwnarw., (IR .uparw./IR .dwnarw.)ns decreased an average of 0.6% for every hour ending at 0900 to 1800 **EST**. Differences (DIFR) between measured IR .uparw./IR .dwnarw. and that predicted with the ns regressions for each hour were regressed on a characteristic soil moisture potential (.psi.sm) for the dune sand and on a ratio of calculated actual to potential evapotranspiration (EC/PET) for the Typic Argiaquoll. Correlations of DIFR on .psi.sm or ET/PET were low. Differences in reflectance first appeared to increase with increasing moisture stress, and then decreased with further increase in moisture stress, as leaf rolling reduced the RGPC. These findings suggest one reason for different IR reflectance-plant moisture stress results reported in the literature, and clearly show that without accurate measures of LAI (or RGPC) and IR .dwnarw. plant moisture stress **cannot** be detected with measurements of IR .uparw..

L3 ANSWER 50 OF 55 MEDLINE DUPLICATE 26
ACCESSION NUMBER: 82134716 MEDLINE
DOCUMENT NUMBER: 82134716 PubMed ID: 6120690
TITLE: Genetic and biochemical studies of the highly active esterases A' and B associated with organophosphate resistance in mosquitoes of the Culex pipiens complex.
AUTHOR: Pasteur N; Iseki A; Georghiou G P
SOURCE: BIOCHEMICAL GENETICS, (1981 Oct) 19 (9-10) 909-19. Journal code: 0126611. ISSN: 0006-2928.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198204
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19950206
Entered Medline: 19820412

AB The highly active esterases A' and B that **cannot** be dissociated from OP resistance in Culex pipiens from France and California are shown to have equivalent Km values (2.1 x 10(-6) M/min/mosquito) but different turnover rates (Vm = 2.13 and 0.57 x 10(-6) M/min/mosquito, respectively) and pH for maximum activity. Both enzymes have broad substrate specificities and at least one, esterase A', can hydrolyze OP insecticides. In addition, esterases A' and B are coded by two closely linked genes, **Est**-3 and **Est**-2, respectively (0.67 unit of crossing over), located on the same autosome as pl, a locus attributed to linkage group III. The estimated distance between **Est**-2 and pl was 9.4 units.

L3 ANSWER 51 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1982:192134 BIOSIS
DOCUMENT NUMBER: BA73:52118
TITLE: SOCIAL GROUPING AND GENETIC VARIATION IN COMMON SHINERS NOTROPIS-CORNUTUS PISCES CYPRINIDAE.
AUTHOR(S): FERGUSON M M; NOAKES D L G
CORPORATE SOURCE: DEP. ZOOL., UNIV. GUELPH, GUELPH, ONT. N1G 2W1, CAN.

SOURCE: ENVIRON BIOL FISHES, (1981) 6 (3-4), 357-360.
CODEN: EBFID3. ISSN: 0378-1909.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Heterogeneous gene frequencies of **Est**-1 across groups of N. cornutus provide evidence of behaviorally imposed restrictions on stock structuring. Positive fixation indices (F1S = 0.056 and F1T = 0.085) were reflected by a deficiency of heterozygotes for pooled groups. The degree of subdivision of N. cornutus stocks **cannot** be evaluated with the present evidence but it is likely that their schooling behavior is associated with significant genotypic structuring of the species.

L3 ANSWER 52 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1982:208178 BIOSIS
DOCUMENT NUMBER: BA73:68162
TITLE: CORRELATED RESPONSES TO SELECTION FOR WING LENGTH IN ALLOZYME SYSTEMS OF DROSOPHILA-MELANOGASTER.
AUTHOR(S): AGUADE M; CUELLO J; PREVOSTI A
CORPORATE SOURCE: DEP. GENET., FAC. BIOL., UNIV. BARCELONA, BARCELONA-7, SPAIN.
SOURCE: THEOR APPL GENET, (1981) 60 (5), 317-327.
CODEN: THAGA6. ISSN: 0040-5752.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Significant changes of genotypic structure in 20 lines selected for wing length are detected by analysis of the allelic frequencies of several enzyme loci (XDH, LAP-D, **EST**-6, 1-APH, ADH, .alpha.-GPDH). These changes are not haphazard but a consequence of the effects of selection on the genetic structure of the population, since replicate lines always behave in a parallel way. The changes are larger in the lines selected for short wings, in which the genetic variability decreases considerably. This decrease is the result of selection for homozygosity, detected at the allozyme loci, but most probably reflects homozygosity of more or less extended chromosomal segments. Selection for wing length, especially for short wings, favored recombinants of the initial founder chromosomes. Only in the 1-APH and the **EST**-6 loci, separated by 11.7 centimorgans on the genetic map, do the alleles linked in the founder lines change in parallel in the control and long wing lines. The correlated response in the allozyme allele frequencies **cannot** be accounted for by a direct influence of the allozymes on the variability in wing length. The changes in the **EST**-6, 1-APH and perhaps in the LAP-D, can be explained by a direct effect of natural selection on the allozyme loci, probably in interaction with the effect of selection for wing length on linked loci. This last effect seems to be the main factor contributing to the change detected in the XDH locus.

L3 ANSWER 53 OF 55 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 81078629 MEDLINE
DOCUMENT NUMBER: 81078629 PubMed ID: 6777865
TITLE: A gamma 1 heavy-chain disease protein *EST) lacking the entire VH and CH1 domains.
AUTHOR: Biewenga J; Frangione B; Franklin E C; van Loghem E
SOURCE: SCANDINAVIAN JOURNAL OF IMMUNOLOGY, (1980) 11 (6) 601-7.
Journal code: 0323767. ISSN: 0300-9475.
Report No.: NASA-81078629.
PUB. COUNTRY: Norway
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 198102
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19900316
Entered Medline: 19810224

AB A gamma 1 heavy-chain disease protein (**EST**) is described which lacks the entire VH and CH1 domains and starts with the normal sequence of gamma 1 H-chains corresponding to the beginning of the hinger region (position 216). Although degradation **cannot** be excluded with certainty, it is probable that this protein is synthesized as an internally deleted gamma heavy-chain disease protein. Presumably a DNA recombination has occurred resulting in the deletion of the genes of coding for the VH and CH1 domains with splicing of the precursor RNA to the sequence coding for the hinge region.

L3 ANSWER 54 OF 55 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 80135172 MEDLINE
DOCUMENT NUMBER: 80135172 PubMed ID: 535729
TITLE: The genetics of Drosophila subobscura populations. IX. Studies on linkage disequilibrium in four natural populations.
AUTHOR: Loukas M; Krimbas C B; Vergini Y
SOURCE: GENETICS, (1979 Oct) 93 (2) 497-523.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198005
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 19900315
Entered Medline: 19800530

AB Gametic frequencies were obtained in four natural populations of D. sub-obscura by extracting wild chromosomes and subsequently analyzing them for inversions and allozymes. The genes Lap and Pept-1, both located within the same inversions of chromosome O, were found in striking nonrandom associations with them of the same kind and degree in all populations studied. On the contrary, the gene Acph, also located within the previously mentioned inversions, was found in linkage disequilibrium with them only in two populations and of opposite directions. This is also the case for the genes **Est**-9 and Hk, both located within chromosome E inversions. While the gene **Est**-9 was in strong linkage disequilibrium with the inversions, of the same kind and degree in all populations studied, Hk was found to be in linkage equilibrium. Allele frequencies for the 29 genes studied do not show geographical variation except for the genes Lap, Pept-1 and **Est**-9, the ones found in linkage disequilibria with the geographically varying gene arrangements. Although mechanical or historical explanations for these equilibria **cannot** be ruled out, these data **cannot** be explained satisfactorily by the "middle gene explanation," which states that loci displaying such linkage disequilibria are the ones located near the break points of inversions, while the ones displaying linkage equilibria with them are located in the middle of them. There is no evidence for consistent linkage disequilibria between pairs of loci, except for the closely linked genes of the complex locus, **Est**-9. This would

imply, if it is not a peculiarity of the **Est**-9 complex, that the linkage disequilibria are found only between very closely linked loci or that, for less closely linked genes, the associations are too weak to be detected by the usual samples sizes.

L3 ANSWER 55 OF 55 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1979:142692 BIOSIS
DOCUMENT NUMBER: BA67:22692
TITLE: ISO ENZYMES AND MIGRATION IN THE AFRICAN ARMYWORM SPODOPTERA-EXEMPTA LEPIDOPTERA NOCTUIDAE.
AUTHOR(S): DEN BOER M H
CORPORATE SOURCE: DEP. POPUL. EVOL. BIOL., UNIV. UTR., PADUALAAN 8, UTRECHT, NETH.
SOURCE: J ZOOL (LOND), (1978) 185 (4), 539-554.
CODEN: JZOOAE. ISSN: 0022-5460.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Techniques for the separation of proteins have proved to be powerful tools in the study of genetic variation. Polymorphisms on protein levels can be used to study the structure of populations. In general, differences in allele frequencies can be found among populations in different parts of the distribution area of a species. If enough gene flow occurs by migration, the whole system can be regarded as 1 panmictic unit and similar frequencies can be expected in the whole area. African armyworms are caterpillars of the noctuid moth S. exempta. They live on all sorts of graminaceous plants on which vast outbreaks can occur. Their economic importance can be considerable since they eat the main human food crops as well as pasture grasses. The occurrence of migration in S. exempta is known but its importance is a main controversial point. Outbreaks move during the year. These outbreaks could be caused by migrating animals or by increasing local populations when conditions are favorable. The relative importance of migration was determined. Allele frequencies have been determined of 6 alleloenzymes that proved to be genetically polymorphic, an **EST** [esterase], .beta.-HBDH [.beta.-hydroxybutyrate dehydrogenase], ODH [octanol dehydrogenase], .alpha.-GPDH [.alpha.-glycerophosphate dehydrogenase], ME [malic enzyme] and LDH [lactate dehydrogenase]. Armyworm samples (17) were collected at a maximal distance of 2000 km in Kenya, Tanzania and Rhodesia on different food plants during 1975 and 1976. No heterogeneity among these samples could be detected in allele frequencies. A comparison with data from relevant literature on insects showed that the lack of heterogeneity **cannot** be described to inadequacy of the data. The occurrence of extensive migration causes the similarity in allele frequencies.

=> d history

(FILE 'HOME' ENTERED AT 11:50:48 ON 09 JUL 2002)

FILE 'MEDLINE, BIOSIS' ENTERED AT 11:51:25 ON 09 JUL 2002
L1 14581 S EST# OR (SEQUENCE(W)TAG#)
L2 83 S L1(S)("NOT" OR CANNOT)
L3 55 DUP REM L2 (28 DUPLICATES REMOVED)

=> s EST or ESTs or (sequence(w)tag#)
L4 13496 EST OR ESTS OR (SEQUENCE(W) TAG#)

```
=> s l2 (s)("not" or cannot)
L5          83 L2 (S)("NOT" OR CANNOT)

=> s l4 (s)("not" or cannot)
L6          82 L4 (S)("NOT" OR CANNOT)

=> log h
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                      51.84      52.05

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 11:56:18 ON 09 JUL 2002


Welcome to STN International!  Enter x:x

LOGINID:ssspta1600kxc

PASSWORD:
 * * * * * * RECONNECTED TO STN INTERNATIONAL * * * * * *
SESSION RESUMED IN FILE 'MEDLINE, BIOSIS' AT 12:04:49 ON 09 JUL 2002
FILE 'MEDLINE' ENTERED AT 12:04:49 ON 09 JUL 2002
FILE 'BIOSIS' ENTERED AT 12:04:49 ON 09 JUL 2002
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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                      51.84      52.05

=> s mRNA or cDNA or polynucleotide# or DNA or transcript#
L7     1637565 MRNA OR CDNA OR POLYNUCLEOTIDE# OR DNA OR TRANSCRIPT#

=> s mRNA or cDNA or polynucleotide# or transcript#
L8      544939 MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#

=> s l8(s)(expression(w)pattern#)
L9       11399 L8(S)(EXPRESSION(W) PATTERN#)

=> s l9(s)(cannot or "not")
L10         90 L9(S)(CANNOT OR "NOT")

=> dup rem l10
PROCESSING COMPLETED FOR L10
L11          51 DUP REM L10 (39 DUPLICATES REMOVED)

=> d ibib abs tot

L11  ANSWER 1 OF 51     MEDLINE                          DUPLICATE 1
ACCESSION NUMBER:   2002324987     IN-PROCESS
DOCUMENT NUMBER:    22062809   PubMed ID: 12067990
TITLE:              Parallel analysis of sporadic primary ovarian carcinomas
by
                    spectral karyotyping, comparative genomic hybridization,
                    and expression microarrays.
AUTHOR:             Bayani Jane; Brenton James D; Macgregor Pascale F;
Beheshti
                    Ben; Albert Monique; Nallainathan Dhani; Karaskova Jana;
                    Rosen Barry; Murphy Joan; Laframboise Stephanie; Zanke
                    Brent; Squire Jeremy A
```

CORPORATE SOURCE: Ontario Cancer Institute [J. B., B. B., D. N., J. K., B. Z., J. A. S.] and Departments of Medical Oncology and Hematology [J. D. B., B. Z.] and Gynecological Oncology [B. R., J. M., S. L.], Princess Margaret Hospital, University Health Network.
SOURCE: CANCER RESEARCH, (2002 Jun 15) 62 (12) 3466-76. Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020618
Last Updated on STN: 20020618

AB Analysis of ovarian carcinomas has shown that karyotypes are often highly abnormal and **cannot** be identified with certainty by conventional cytogenetic methods. In this study, 17 tumors derived from 13 patients were analyzed by a combination of spectral karyotyping (SKY), comparative genomic hybridization (CGH), and expression microarrays. Within the study group, a total of 396 chromosomal rearrangements could be identified by SKY and CGH analysis. When the distribution of aberrations was normalized with respect to relative genomic length, chromosomes 3, 8, 11, 17, and 21 had the highest frequencies. Parallel microarray expression studies of 1718 human **cDNAs** were used to analyze expression profiles and to determine whether correlating gene expression with chromosomal rearrangement would identify smaller subsets of differentially expressed genes. Within the entire set of samples, microarray expression analysis grouped together poorly differentiated tumors irrespective of histological subtype. For three patients, a comparison between genomic alterations and gene **expression pattern** was performed on samples of primary and metastatic tumors. Their common origin was demonstrated by the close relationship of both the SKY and CGH karyotypes and the observed profiles of gene expression. In agreement with the pattern of genomic imbalance observed for chromosome 3 in ovarian cancer, the relative expression profile with respect to a normal ovary exhibited a contiguous pattern of reduced expression of genes mapping to the 3p25.5-3p21.31 and increased expression of genes from 3q13.33-3q28. This study demonstrates that SKY, CGH, and microarray analysis can in combination identify significantly smaller subsets of differentially expressed genes for future studies.

L11 ANSWER 2 OF 51 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002149978 MEDLINE
DOCUMENT NUMBER: 21876771 PubMed ID: 11882461
TITLE: Expression of estrogen receptor alpha and beta in the epiphyseal plate of the rat.
AUTHOR: van der Eerden B C J; Gevers E F; Lowik C W G M; Karperien M; Wit J M
CORPORATE SOURCE: Department of Pediatrics, Leiden University Medical Center, Leiden, The Netherlands.. b.c.j.van_der_eerden@lumc.nl
SOURCE: BONE, (2002 Mar) 30 (3) 478-85. Journal code: 8504048. ISSN: 8756-3282.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206

ENTRY DATE: Entered STN: 20020308
Last Updated on STN: 20020625
Entered Medline: 20020624

AB In this study we examine the spatial and temporal expression of estrogen receptor (ER) alpha and beta **mRNA** and protein in the tibial growth plate of the rat after birth, as well as the hormonal regulation of their expression. Using in situ hybridization and immunohistochemistry, we demonstrated ER alpha and ER beta **mRNA** and protein in tibial growth plates from 1 to 40 weeks after birth. ER alpha and beta **mRNA** and protein were localized in late proliferating and early hypertrophic chondrocytes during early life (1 and 4 weeks of age), whereas the immunohistochemistry also showed staining for ER alpha and beta in the resting cells. A similar **expression pattern** was observed during sexual maturation (7 weeks of age) except that ER beta **mRNA** was also detected in early proliferating chondrocytes. After sexual maturation (from 12 up to 40 weeks of age) ER alpha and beta **mRNA** and protein expression was confined to late proliferating and early hypertrophic chondrocytes. Apart from a relatively higher ER alpha **mRNA** expression in males after sexual maturation, we did not detect differences in expression of ERs between genders. Expression of ER beta **mRNA** in epiphyseal plates was increased in growth-retarded hypophysectomized rats compared with controls. Administration of growth hormone (GH) did not reverse the increased ER expression to normal. These data suggest that ER alpha and beta are coexpressed in growth plates of the rat after birth and that the level of expression of ERs in these tissues is hormonally regulated. Furthermore, our data indicate that the absence of growth-plate closure in the rat **cannot** be explained by disappearance of ER alpha expression during sexual maturation per se.

L11 ANSWER 3 OF 51 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002204653 IN-PROCESS
DOCUMENT NUMBER: 21935105 PubMed ID: 11937754
TITLE: Renal transcriptomes: segmental analysis of differential expression.
AUTHOR: Elalouf J-M; Aude J-C; Billon E; Cheval L; Doucet A; Virlon B
CORPORATE SOURCE: Departement de Biologie Cellulaire et Moleculaire, Service de Biologie Cellulaire, CNRS URA 1859, CEA SACLAY, Gif-sur-Yvette, France.
SOURCE: EXPERIMENTAL NEPHROLOGY, (2002) 10 (2) 75-81.
Journal code: 9302239. ISSN: 1018-7782.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020409
Last Updated on STN: 20020409

AB Background/Aims: Progress accomplished by complete genomes and **cDNA**-sequencing projects calls for methods that fully use these resources to study gene **expression patterns** in characterized cell populations. However, since the number of functional genes **cannot** be readily inferred from the genomic sequence, it is highly desirable to make use of methods enabling to study both known and unknown genes. Methods: The method of serial analysis of gene expression provides short diagnostic **cDNA** tags without bias towards known genes. In addition, the frequency of each tag in the library

conveys quantitative information on gene expression. A microassay was set-up to perform serial analysis of gene expression in minute samples such as those obtained by microdissecting nephron segments. Results: Studies carried out in the thick ascending limb of Henle's loop and the collecting duct of the mouse kidney provided expression data for several thousand genes. Known markers were found appropriately enriched, and several of the thick ascending limb or collecting duct specific **transcripts** had no database match. Conclusions: The microassay for serial analysis of gene expression makes possible large-scale quantitative measurements of **mRNA** levels in nephron segments. The comprehensive picture generated by analyzing both known and unknown **transcripts** in defined cell populations should help to discover genes with dedicated functions.

L11 ANSWER 4 OF 51 MEDLINE
ACCESSION NUMBER: 2002151656 IN-PROCESS
DOCUMENT NUMBER: 21880379 PubMed ID: 11883525
TITLE: Gene expression in inherited breast cancer.
AUTHOR: Hedenfak Ingrid A; Ringner Markus; Trent Jeffrey M; Borg Ake
CORPORATE SOURCE: Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, Maryland 20892, USA.
SOURCE: ADVANCES IN CANCER RESEARCH, (2002) 84 1-34.
Journal code: 0370416. ISSN: 0065-230X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020311
Last Updated on STN: 20020311

AB Large proportions of hereditary breast cancers are due to mutations in the two breast cancer susceptibility genes BRCA1 and BRCA2. Considerable effort has gone into studying the function(s) of these tumor suppressor genes, both in attempts to better understand why individuals with these inherited mutations acquire breast (and ovarian) cancer and to potentially develop better treatment strategies. The advent of tools such as **cDNA** microarrays has enabled researchers to study global gene **expression patterns** in, for example, primary tumors, thus providing more comprehensive overviews of tumor development and progression. Our recent study (Hedenfalk et al., 2001) strongly supports the principle that genomic approaches to classification of hereditary breast cancers are possible, and that further studies will likely identify the most significant genes that discriminate between subgroups and may influence prognosis and treatment. A large number of hereditary breast cancer cases **cannot** be accounted for by mutations in these two genes and are believed to be due to as yet unidentified breast cancer predisposition genes (BRCAx). Subclassification of these non-BRCA1/2 breast cancers using **cDNA** microarray-based gene expression profiling, followed by linkage analysis and/or investigation of genomic alterations, may help in the recognition of novel breast cancer predisposition loci. To summarize, gene expression-based analysis of hereditary breast cancer can potentially be used for classification purposes, as well as to expand upon our knowledge of differences between different forms of hereditary breast cancer. Initial studies indicate that

a patient's genotype does in fact leave an identifiable trace on her/his cancer's gene expression profile.

L11 ANSWER 5 OF 51 MEDLINE
ACCESSION NUMBER: 2001680496 MEDLINE
DOCUMENT NUMBER: 21583607 PubMed ID: 11726618
TITLE: Changes in mRNA levels of the Myoc/Tigr gene in the rat eye
after experimental elevation of intraocular pressure or optic nerve transection.
AUTHOR: Ahmed F; Torrado M; Johnson E; Morrison J; Tomarev S I
CORPORATE SOURCE: Laboratory of Molecular and Developmental Biology, National
Eye Institute/NIH, Building 6, 6 Center Drive MSC 2730, Bethesda, MD 20892-2730, USA.
SOURCE: INVESTIGATIVE OPHTHALMOLOGY AND VISUAL SCIENCE, (2001 Dec) 42 (13) 3165-72.
Journal code: 7703701. ISSN: 0146-0404.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011203
Last Updated on STN: 20020125
Entered Medline: 20020115

AB PURPOSE: To isolate the rat Myoc/Tigr gene and investigate changes in its **expression pattern** in normal eyes and in eyes with either pressure-induced optic nerve damage or optic nerve transection. METHODS: **Expression pattern** of the rat Myoc/Tigr gene was investigated by Northern blot hybridization. Optic nerve damage and death of ganglion cells in the retina were induced unilaterally, by injection of hypertonic saline solution, episcleral vein cauterization, or optic nerve transection. The levels of **mRNA** for Myoc/Tigr were compared between several tissues of the control and surgically altered eyes, by using semiquantitative RT-PCR, real-time PCR, and Northern blot analysis. RESULTS: The rat Myoc/Tigr gene is 10 kb long and contains three exons. Among the eye tissues analyzed, Myoc/Tigr **mRNA** was detected in the combined tissues of the eye angle, sclera, cornea, retina, and optic nerve head. With pressure-induced optic nerve degeneration, the level of Myoc/Tigr **mRNA** decreased in the retina and the combined tissues of the eye angle, but increased in the optic nerve head. After optic nerve transection, the level of Myoc/Tigr **mRNA** increased in the retina, but did not change in the combined tissues of the eye angle. CONCLUSIONS: The decreased level of Myoc/Tigr **mRNA** in the retina after induction of elevated intraocular pressure compared with that in the control retina **cannot** be explained by ganglion cell death alone. Differences in Myoc/Tigr **mRNA** levels in eye tissues after elevation of intraocular pressure or optic nerve transection may reflect the activation of different signaling pathways involved in regulation of this gene.

L11 ANSWER 6 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:487277 BIOSIS
DOCUMENT NUMBER: PREV200100487277
TITLE: Expression of myelin/oligodendrocyte glycoprotein isoforms in humans.

AUTHOR(S): Allamargot, C. (1); Gardinier, M. V. (1)
CORPORATE SOURCE: (1) Pharmacology, University of Iowa, Iowa City, IA USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 411. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Myelin/oligodendrocyte glycoprotein (MOG) is a CNS-specific integral membrane protein found on oligodendrocyte cell bodies, their processes and the outermost layer of the myelin sheath. Only a single MOG **mRNA** encoding a 25.1 kDa protein was found initially (cow, mouse, rat). Sequence analysis of human MOG **cDNAs** suggested a single alternative splice product, and RT-PCR analyses revealed eight distinct alternatively spliced **mRNA transcripts**. Among these **cDNAs**, two previously undiscovered exons were found. We have also confirmed that a number of these isoforms are expressed in baboon brain **mRNA**. The splice variants all differ within MOG's C-terminal cytoplasmic domain. We are currently investigating the expression of these proteins in human CNS tissue. As the currently available MOG antibodies (Abs) **cannot** distinguish between MOG25.1 and the other forms, peptide antigens representing areas encoded by the novel exons or discrete splice junctions in the MOG **transcripts** were designed and domain-specific Abs were made. Ab specificity was tested on N20.1 oligodendrocytes that do not express MOG endogenously, and on N20 cells stably transfected with MOG variants. Four peptide Abs recognize different subsets of MOG isoforms; three peptide Abs each recognize a specific isoform. Preliminary immunohistochemical studies using human tissues reveal that all eight MOG isoforms could be expressed in adult CNS. Besides MOG25.1, MOG22.7, MOG20.2 and MOG16.3 have been specifically identified. We are now investigating developmental and spatial **expression patterns** of these proteins.

L11 ANSWER 7 OF 51 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2001552455 MEDLINE
DOCUMENT NUMBER: 21485152 PubMed ID: 11599658
TITLE: Independent patterns of cytochrome P450 gene expression in liver and blood in patients with suspected liver disease.
AUTHOR: Finnstrom N; Thorn M; Loof L; Rane A
CORPORATE SOURCE: Department of Medical Laboratory Sciences and Technology, Karolinska Institute, Huddinge University Hospital, Stockholm, Sweden.. Niklas.Finnstrom@labtek.ki.se
SOURCE: EUROPEAN JOURNAL OF CLINICAL PHARMACOLOGY, (2001 Aug) 57 (5) 403-9.
Journal code: 1256165. ISSN: 0031-6970.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20011016
Last Updated on STN: 20020412
Entered Medline: 20020410

AB OBJECTIVE: Assessment of liver metabolism using blood samples was tested

by comparison of cytochrome P450 (CYP) gene expression in paired liver and blood samples from 13 individuals. METHODS: Total RNA was isolated from percutaneous needle biopsies and blood collected simultaneously. Gene expression for CYP1A2, CYP1B1, CYP2E1 and CYP3A4 was studied using a real-time reverse-transcription polymerase chain reaction (RT-PCR) method.
RESULTS: All CYP **mRNA** species were expressed in all liver biopsies but at varying levels. The highest and lowest levels of expression were observed for CYP2E1 and CYP1B1, respectively. The **expression patterns** differed between blood and liver. CYP1B1 was expressed in all blood samples at a 20% higher level than in the liver. CYP1A2, CYP2E1 and CYP3A4 were expressed in blood at 35- to 5,000-fold lower levels than in liver. None of the **transcripts** in blood showed any correlation with the expression in liver. CONCLUSION: We conclude that blood **cannot** serve as a surrogate organ for assessment of the expression of the studied CYP genes in liver.

L11 ANSWER 8 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:426316 BIOSIS
DOCUMENT NUMBER: PREV200100426316
TITLE: Molecular analysis of differentially expressed genes during postharvest deterioration in cassava (Manihot esculenta Crantz) tuberous roots.
AUTHOR(S): Huang, Jiang; Bachem, Christian; Jacobsen, Evert; Visser, Richard G. F. (1)
CORPORATE SOURCE: (1) Laboratory of Plant Breeding, Department of Plant Sciences, The Graduate School of Experimental Plant Science (EPS), Wageningen University, 6700 AJ, Wageningen Netherlands
SOURCE: Euphytica, (2001) Vol. 120, No. 1, pp. 85-93. print. ISSN: 0014-2336.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB One of the major problems for cassava is the rapid deterioration after harvesting cassava tuberous roots, which limits the possibilities for production and distribution of cassava in the world. Postharvest deterioration is an inherent problem for cassava since wounding and mechanical damage of the tuberous roots **cannot** be prevented during harvesting, which includes postharvest physiological deterioration (PPD) and secondary deterioration. To date, the molecular mechanism and biochemical pathways of PPD are poorly understood. The aim of this project, which is focusing on the early stages (first 72 hrs), is to gain molecular insight and identify important metabolic pathways during the process of PPD in cassava tuberous roots. Finally by reverse genetic approaches to delay or even prevent the process of PPD in cassava tuberous roots. By using a new RNA fingerprinting method, called **cDNA** -AFLP, we have screened more than 6,000 TDFs (**Transcript** Derived Fragments) via up to 100 primer combinations during the early process of PPD in cassava. Only 10% of the TDFs are developmentally regulated, while the other 90% are expressed throughout the process of PPD in cassava tuberous roots. Furthermore, in order to set up a functional catalogue of differentially expressed genes during PPD, 70 TDFs were selected and isolated based on their **expression patterns**, which were either up-regulated, down-regulated or transiently induced. Around 40 of these TDFs were found to be similar with known genes in databases. The

other 30 TDFs were present mostly genes without known function. Through data analysis, it is shown that important biochemical and physiological processes, such as notably oxygen stress, carbohydrate metabolism, protein metabolism and phenolic compounds synthesis, are involved in PPD in cassava tuberous roots.

L11 ANSWER 9 OF 51 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2001147775 MEDLINE
DOCUMENT NUMBER: 21066000 PubMed ID: 11137440
TITLE: Angiotensin receptor(s) in fowl.
AUTHOR: Kempf H; Corvol P
CORPORATE SOURCE: INSERM U36 and College de France, 3 rue d'Ulm, 75005, Paris, France.. hkempf@infobiogen.fr
SOURCE: COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY. PART A, MOLECULAR AND INTEGRATIVE PHYSIOLOGY, (2001 Jan) 128 (1) 77-88.
Ref: 40
Journal code: 9806096. ISSN: 1095-6433.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010315

AB The cloning of the avian Ang II receptor shows that it is molecularly close to the AT(1)-type mammalian receptor. However, pharmacological characterization in transfected cells shows that, even though the avian receptor is coupled to the phospholipase C, as is the AT(1), its profile of specificity towards antagonists appears different from that of the two angiotensin II mammalian receptor types. The fowl Ang II receptor **mRNA** is expressed in classical adult target organs for Ang II and, interestingly, also in endothelial cells, but not in vascular smooth muscle cells. In the endothelial cells, it may mediate the peculiar vasorelaxation effect of Ang II already reported in the chicken. The recent description of the **expression pattern** in the chick embryo shows that the avian Ang II receptor is expressed in many different mesenchymal tissues, a feature which is the signature of the AT(2) mammalian receptor. Altogether, these data imply that the avian Ang II receptor is an atypical receptor that **cannot** be readily classified as either of the two mammalian Ang II receptor types and, therefore, reinforce the evidence for another Ang II receptor in the avian class.

L11 ANSWER 10 OF 51 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2001200193 MEDLINE
DOCUMENT NUMBER: 21184103 PubMed ID: 11287179
TITLE: Mice with a homozygous gene trap vector insertion in mgcRacGAP die during pre-implantation development.
AUTHOR: Van de Putte T; Zwijsen A; Lonnoy O; Rybin V; Cozijnsen M; Francis A; Baekelandt V; Kozak C A; Zerial M; Huylebroeck D
CORPORATE SOURCE: Department of Cell Growth, Differentiation and Development (VIB-07), Flanders Interuniversity Institute for Biotechnology (VIB) and Laboratory of Molecular Biology (CELGEN), University of Leuven, Herestraat 49, 3000,

Leuven, Belgium.
SOURCE: MECHANISMS OF DEVELOPMENT, (2001 Apr) 102 (1-2) 33-44.
Journal code: 9101218. ISSN: 0925-4773.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010820
Last Updated on STN: 20010820
Entered Medline: 20010816

AB In a phenotypic screen in mice using a gene trap approach in embryonic stem cells, we have identified a recessive loss-of-function mutation in the mgcRacGAP gene. Maternal protein is present in the oocyte, and mgcRacGAP gene transcription starts at the four-cell stage and persists throughout mouse pre-implantation development. Total mgcRacGAP deficiency results in pre-implantation lethality. Such E3.5 embryos display a dramatic reduction in cell number, but undergo compaction and form a blastocoel. At E3.0-3.5, binucleated blastomeres in which the nuclei are partially interconnected are frequently observed, suggesting that mgcRacGAP is required for normal mitosis and cytokinesis in the pre-implantation embryo. All homozygous mutant blastocysts fail to grow out on fibronectin-coated substrates, but a fraction of them can still induce decidual swelling in vivo. The mgcRacGAP **mRNA expression pattern** in post-implantation embryos and adult mouse brain suggests a role in neuronal cells. Our results indicate that mgcRacGAP is essential for the earliest stages of mouse embryogenesis, and add evidence that CYK-4-like proteins also play a role in microtubule-dependent steps in the cytokinesis of vertebrate cells. In addition, the severe phenotype of null embryos indicates that mgcRacGAP is functionally non-redundant and **cannot** be substituted by other GAPs during early cleavage of the mammalian embryo.

L11 ANSWER 11 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:324361 BIOSIS
DOCUMENT NUMBER: PREV200200324361
TITLE: Cre reporter strains produced by targeted insertion of EYFP and ECFP into the ROSA26 locus.
AUTHOR(S): Srinivas, Shankar; Watanabe, Tomoko; Lin, Chyuan-Sheng; William, Chris M.; Tanabe, Yasuto; Jessell, Thomas M.; Costantini, Frank (1)
CORPORATE SOURCE: (1) Department of Genetics and Development, Columbia University, New York, NY: shankar@srinivas.org, tw118@columbia.edu, cs15@columbia.edu, cmw3@columbia.edu, yt48@columbia.edu, tmj1@columbia.edu, fdc3@columbia.edu USA
SOURCE: BMC Developmental Biology, (March 27, 2001) Vol. 1, No. 4 Cited April 14, 2002, pp. 1-8. http://www.biomedcentral.com/content/pdf/1471-213X-1-4.pdf cited May 7, 2002 http://www.biomedcentral.com/1471-213X. online.
ISSN: 1471-213X.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Background: Several Cre reporter strains of mice have been described, in which a lacZ gene is turned on in cells expressing Cre recombinase, as well as their daughter cells, following Cre-mediated excision of a loxP-flanked transcriptional "stop" sequence. These mice are useful for cell lineage tracing experiments as well as for monitoring the expression

of Cre transgenes. The green fluorescent protein (GFP) and variants such as EYFP and ECFP offer an advantage over lacZ as a reporter, in that they can be easily visualized without recourse to the vital substrates required to visualize beta-gal in living tissue. Results: In view of the general utility of targeting the ubiquitously expressed ROSA26 locus, we constructed a generic ROSA26 targeting vector. We then generated two reporter lines of mice by inserting EYFP or ECFP **cDNAs** into the ROSA26 locus, preceded by a loxP-flanked stop sequence. These strains were tested by crossing them with transgenic strains expressing Cre in a ubiquitous (beta-actin-Cre) or a cell-specific (IslI-Cre and EnI-Cre) pattern. The resulting EYFP or ECFP **expression patterns** indicated that the reporter strains function as faithful monitors of Cre activity. Conclusions: In contrast to existing lacZ reporter lines, where lacZ expression **cannot** easily be detected in living tissue, the EYFP and ECFP reporter strains are useful for monitoring the expression of Cre and tracing the lineage of these cells and their descendants in cultured embryos or organs. The non-overlapping emission spectra of EYFP and ECFP make them ideal for double labeling studies in living tissues.

L11 ANSWER 12 OF 51 MEDLINE
ACCESSION NUMBER: 2000469607 MEDLINE
DOCUMENT NUMBER: 20309050 PubMed ID: 10852210
TITLE: A new member of acid-sensing ion channels from pituitary gland.
AUTHOR: Grunder S; Geissler H S; Bassler E L; Ruppersberg J P
CORPORATE SOURCE: Department of Otolaryngology, Section of Sensory Biophysics, Tubingen, Germany.
SOURCE: NEUROREPORT, (2000 Jun 5) 11 (8) 1607-11. Journal code: 9100935. ISSN: 0959-4965.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF013598; GENBANK-AJ242554; GENBANK-AJ271642; GENBANK-AJ271643; GENBANK-U53211; GENBANK-U94403
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001012
Last Updated on STN: 20001012
Entered Medline: 20001005

AB Acid-sensing ion channels (ASICs) constitute a branch of the super-gene family of amiloride-sensitive sodium channels. So far five different ASICs have been cloned from mammalian tissues. They are activated by a drop of extracellular pH but differ with respect to effective agonist concentration, desensitization and **mRNA expression pattern**. Here we report cloning of ASIC4, a new protein showing about 45% identity to other ASICs. ASIC4 is 97% identical between rat and human and shows strongest expression in pituitary gland. Moreover, we detected expression throughout the brain, in spinal cord, and inner ear. ASIC4 **cannot** be activated by a drop of extracellular pH in Xenopus oocytes, suggesting association with other subunits or activation by a ligand different from protons. Our results suggest a role for ASICs also in endocrine glands.

L11 ANSWER 13 OF 51 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001009671 MEDLINE
DOCUMENT NUMBER: 20331587 PubMed ID: 10875332
TITLE: Nodule-expressed Cyp15a cysteine protease genes map to

syntenic genome regions in Pisum and Medicago spp.
AUTHOR: Vincent J L; Knox M R; Ellis T H; Kalo P; Kiss G B; Brewin N J
CORPORATE SOURCE: Department of Genetics, John Innes Centre, Norwich Research Park, UK.
SOURCE: MOLECULAR PLANT-MICROBE INTERACTIONS, (2000 Jul) 13 (7) 715-23.
Journal code: 9107902. ISSN: 0894-0282.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ245868; GENBANK-AJ250432
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001026

AB PsCyp15a is a gene that encodes a vacuolar cysteine protease expressed in wilt-induced shoots of Pisum sativum (pea) and in root nodules. To further the understanding of nodular PsCyp15a expression, a region 5' to the coding sequence of the gene was cloned. Varying lengths of 5' untranslated sequence were fused with the uidA coding region and introduced from Agrobacterium rhizogenes into "hairy roots" of Vicia hirsuta. In this transgenic root nodulation assay, a promoter sequence of 900 bp was sufficient to give an **expression pattern** indistinguishable from that obtained in pea nodules by in situ hybridization. An orthologue of PsCyp15a was cloned from nodule **mRNA** of Medicago sativa and a corresponding gene identified in M. truncatula was also shown to express strongly in nodules. With molecular mapping techniques, it was demonstrated that these genes map to a syntenic genome location in pea and Medicago spp., but the map positions of the Cyp15a genes **cannot** be correlated with existing nodulation mutants.

L11 ANSWER 14 OF 51 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2000156385 MEDLINE
DOCUMENT NUMBER: 20156385 PubMed ID: 10675629
TITLE: An ascidian glycine-rich RNA binding protein is not induced by temperature stress but is expressed under a genetic program during embryogenesis.
AUTHOR: Tanaka K J; Kawamura H; Matsugu H; Nishikata T
CORPORATE SOURCE: Department of Biology, Faculty of Science, Konan University, 8-9-1 Higashinada-ku, Kobe, Japan.
SOURCE: GENE, (2000 Feb 8) 243 (1-2) 207-14.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000403

AB We have cloned a putative ascidian glycine-rich RNA binding protein gene, CiGRP1. Its maternal **transcript** and protein are stored in the unfertilized egg. They are gradually decreased during the first few rounds

of cleavage. The CiGRP1 zygotic **transcript** and protein start to accumulate at the gastrula stage. The CiGRP1 **transcript** is expressed in the brain precursor and mesenchyme precursor cells of the gastrula and the neurula stage, and the brain and mesenchyme cells of the tailbud stage embryo. The CiGRP1 protein is found in all nuclei and in the cytoplasm of brain and mesenchyme cells. Although many glycine-rich RNA binding protein homologs of plants and vertebrates are cold-inducible, CiGRP1 **cannot** be induced by cold shock or heat shock at the transcriptional and translational levels during embryogenesis. The temporal **expression pattern** and the tissue-restricted **expression pattern** of CiGRP1 suggest that it has important roles in the very early stage of development and in the brain and the mesenchyme tissue specification.

L11 ANSWER 15 OF 51 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2000156381 MEDLINE
DOCUMENT NUMBER: 20156381 PubMed ID: 10675625
TITLE: cDNA cloning, characterization, expression and recombinant protein production of leukemia inhibitory factor (LIF) from the marsupial, the brushtail possum (Trichosurus vulpecula).
AUTHOR: Cui S; Selwood L
CORPORATE SOURCE: Department of Zoology, La Trobe University, Plenty Road, Bundoora, Australia.. S.Cui@zoo.labrobe.edu.au
SOURCE: GENE, (2000 Feb 8) 243 (1-2) 167-78.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000403

AB A reverse transcription technique using RNA templates combined with polymerase chain reaction (RT-PCR) was used to clone the **cDNA** fragment encoding the amino acid sequence of mature LIF protein of the marsupial, the brushtail possum, Trichosurus vulpecula. A PCR product with expected size, of 546bp, and termed tvLIF, was obtained using **cDNA** reverse-transcribed from total RNA isolated from possum uterus. A genomic DNA fragment (about 650bp) between the specified primers was also amplified, indicating the similarity in structure and organization of this gene and LIF genes from studied eutherian species, although the full-length of its **cDNA** and genomic DNA needs to be further clarified. The deduced amino acid sequence of tvLIF shows a high level of sequence identity and similar molecular characteristics to eutherian LIF, which suggests similar biological actions of this molecule in this marsupial. Because the expression of LIF gene in other mammalian species has been found to be at very low levels and its **transcripts** **cannot** be detected by Northern hybridization analysis, the **expression pattern** of tvLIF in adult tissues and reproductive tracts during early development was investigated using the RT-PCR technique. Resultant products of the RT-PCR were further analyzed by Southern hybridization using tvLIF as a probe. tvLIF **transcripts** were detected in most of the adult tissues and in the reproductive tracts of pregnant females. These results lend support to the

idea that LIF contributes to the maintenance of pregnancy in this marsupial.

L11 ANSWER 16 OF 51 MEDLINE
ACCESSION NUMBER: 2000473624 MEDLINE
DOCUMENT NUMBER: 20343713 PubMed ID: 10885299
TITLE: Mutations of the dystrophin gene in dilated cardiomyopathy.
AUTHOR: Shiga N; Akita H; Yokoyama M
CORPORATE SOURCE: First Department of Internal Medicine, Kobe University School of Medicine.
SOURCE: NIPPON RINSHO. JAPANESE JOURNAL OF CLINICAL MEDICINE, (2000
Jan) 58 (1) 123-7. Ref: 20
Journal code: 0420546. ISSN: 0047-1852.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: Japanese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001012
Last Updated on STN: 20001012
Entered Medline: 20001004

AB X-linked dilated cardiomyopathy(XLDCM) is caused by mutations of the dystrophin gene, which was originally cloned as the responsible gene for Duchenne muscular dystrophy and Becker muscular dystrophy. Mutations due to XLDCM are centered on 5' end of the gene, especially M-promoter and the
adjacent region. However, other mutations are dispersed and **cannot** be characterized. Three mechanisms have been proposed by which the involvement of cardiac muscle is so severe in spite of the lack of skeletal muscle symptoms; 1) up-regulation of B- and P-dystrophin in merely skeletal muscle compensating for the defect of M-dystrophin, 2) dysfunction of some parts of dystrophin specifically essential to cardiac muscle, 3) different **expression patterns** of mutant **mRNA** between cardiac and skeletal muscle.

L11 ANSWER 17 OF 51 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2001181872 MEDLINE
DOCUMENT NUMBER: 21098445 PubMed ID: 11173827
TITLE: Cell lines from the same cervical carcinoma but with different radiosensitivities exhibit different cDNA microarray patterns of gene expression.
AUTHOR: Achary M P; Jaggernauth W; Gross E; Alfieri A; Klinger H P;
Vikram B
CORPORATE SOURCE: Department of Radiation Oncology, Albert Einstein College of Medicine of Yeshiva University, and Montefiore Medical Center, Bronx, NY, USA.. achary@aecom.yu.edu
SOURCE: CYTOGENETICS AND CELL GENETICS, (2000) 91 (1-4) 39-43.
Journal code: 0367735. ISSN: 0301-0171.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010329

AB Combining chemotherapy with radiotherapy has improved the cure rate among patients with cancers of the cervix. Although one-half to two-thirds of the patients can be cured by radiation alone, such patients **cannot** be identified at present and must therefore suffer the burden of chemotherapy. Our long-range goal is to identify those cervical cancers that are radiosensitive and could be cured by radiotherapy alone. The advent of methods that permit the simultaneous analysis of **expression patterns** of thousands of genes, make it feasible to attempt to identify the molecular events related to radiosensitivity and the associated regulatory pathways. We hypothesize that the sensitivity of tumor cells to ionizing radiation (IR) is determined by the level of expression of specific genes that may be identified with the aid of **cDNA** microarrays. As the first step in testing this hypothesis, we determined the gene expression differences between two cell lines exhibiting different degrees of radiosensitivity. These were derived from the same tumor prior to treatment from a patient with squamous cell carcinoma of the cervix. The **mRNA** from these cells was subjected to **cDNA** analysis on a microarray of 5,776 known genes and ESTs. The expression of 52 genes of the total of 5,776 was elevated (maximum 4.1 fold) in the radioresistant cells as compared to the radiosensitive cells. Ten of the 52 sequences are known genes while 42 are ESTs. Conversely, the expression of 18 genes was elevated in the sensitive cells as compared to the resistant cells. Seven of these 18 are known genes while eleven are ESTs. Among the genes expressed differentially between the resistant and sensitive cells were several known to be associated with response to IR and many more genes and ESTs that had not previously been reported to be related to radiosensitivity. The genes that showed the greatest overexpression in the radioresistant cell line were metal-regulatory transcription factor-1, cytochrome P450 CYP1B1, adenomatosis polyposis coli, translation elongation factor-1, cytochrome-c oxidase, whereas in the sensitive cell line, transcription factor NF-kappa-B, metalloproteinase inhibitor-1 precursor, superoxide dismutase-2, insulin-like growth factor binding protein-3, guanine nucleotide-binding protein and transforming growth factor beta-induced protein were overexpressed.

L11 ANSWER 18 OF 51 MEDLINE DUPLICATE 11

ACCESSION NUMBER: 2000195154 MEDLINE
DOCUMENT NUMBER: 20195154 PubMed ID: 10733016
TITLE: Mammalian oviduct and protection against free oxygen radicals: expression of genes encoding antioxidant enzymes in human and mouse.
AUTHOR: El Mouatassim S; Guerin P; Menezo Y
CORPORATE SOURCE: Laboratoire Marcel Merieux, Cytogenetique, Lyon, France.
SOURCE: EUROPEAN JOURNAL OF OBSTETRICS, GYNECOLOGY, AND REPRODUCTIVE BIOLOGY, (2000 Mar) 89 (1) 1-6.
Journal code: 0375672. ISSN: 0301-2115.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000518
Last Updated on STN: 20000518

Entered Medline: 20000511

AB Genetic expression of five antioxidant enzymes involved in mechanisms protecting embryos against reactive oxygen species (ROS) was studied in human and mouse oviducts. The presence of **transcripts** encoding for gamma-glutamylcysteine synthetase (GCS), glutathione peroxidase (GPX), Cu-Zn-superoxide dismutase (Cu-Zn-SOD), Mn-superoxide dismutase (Mn-SOD) and catalase was analysed by use of the reverse transcription-polymerase chain reaction (RT-PCR). Different expression profiles of **transcripts** encoding for these enzymes were observed between human and mouse oviducts. In the mouse, all **transcripts** encoding for the enzymes tested were present in oviduct. In human, only **transcripts** encoding for GPX, Cu-Zn-SOD and catalase were also detected in oviduct. However, GCS and Mn-SOD **transcripts** were never observed in human oviduct. Cu-Zn-SOD **transcripts** are relatively highly expressed whatever species. These results suggest that different gene **expression patterns** of these antioxidant enzymes between human and mouse may reflect the variations in the ability of embryos to develop in vivo and in vitro. However, hormone related-expression of the missing **transcripts** in human **cannot** be ruled out.

L11 ANSWER 19 OF 51 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 1999187236 MEDLINE
DOCUMENT NUMBER: 99187236 PubMed ID: 10087076
TITLE: The sexually dimorphic expression of androgen receptors in the song nucleus hyperstriatalis ventrale pars caudale of the zebra finch develops independently of gonadal steroids.
AUTHOR: Gahr M; Metzdorf R
CORPORATE SOURCE: Max-Planck-Institute of Behavioral Physiology, 82319 Seewiesen, Germany.
SOURCE: JOURNAL OF NEUROSCIENCE, (1999 Apr 1) 19 (7) 2628-36. Journal code: 8102140. ISSN: 0270-6474.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199904
ENTRY DATE: Entered STN: 19990426
Last Updated on STN: 19990426
Entered Medline: 19990413

AB The development of sex differences in brain structure and brain chemistry ("brain sex") of vertebrates is frequently thought to depend entirely on gonadal steroids such as androgens and estrogens, which act on the brain at the genomic level by binding to intracellular transcription factors, the androgen receptors (ARs) and estrogen receptors (ERs). These hormone actions are thought to shift the brain from a monomorphic to a dimorphic phenotype. One prominent such example is the nucleus hyperstriatalis ventrale pars caudale (HVc) of the zebra finch (Poephila guttata), a set of cells in the caudal forebrain involved in the control of singing. In contrast with previous studies using nonspecific cell staining techniques, the size and neuron number of the HVc measured by the distribution of AR **mRNA** is already sexually dimorphic on posthatching day (P)9. No ARs or ERs are expressed in the HVc before day 9. Slice cultures of the caudal forebrain of P5 animals show that the sexually dimorphic expression of AR **mRNA** in HVc is independent of the direct action of steroids on this nucleus or any of its immediate presynaptic or postsynaptic partners. Therefore, gonadal steroids do not appear to be

directly involved in the initial sex difference in the **expression pattern** of AR **mRNA**, size, and neuron number of the HVc. Furthermore, we demonstrate that the initial steroid-independent size and its subsequent steroid-independent growth by extension linearly with the extension of the forebrain explains 60-70% of the masculine development of the HVc. Thus, we suggest that epigenetic factors such as the gonadal steroids modify but **cannot** overwrite the sex difference in HVc volume determined autonomously in the brain.

L11 ANSWER 20 OF 51 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 1999274007 MEDLINE
DOCUMENT NUMBER: 99274007 PubMed ID: 10344210
TITLE: A transcript encoding translation initiation factor eIF-5A is stored in unfertilized egg cells of maize.
AUTHOR: Dresselhaus T; Cordts S; Lorz H
CORPORATE SOURCE: Applied Plant Molecular Biology II, University of Hamburg, Germany.
SOURCE: PLANT MOLECULAR BIOLOGY, (1999 Mar) 39 (5) 1063-71. Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y07920
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990618
Last Updated on STN: 19990618
Entered Medline: 19990604

AB Differential screening of **cDNA** libraries of unfertilized egg cells and in vitro zygotes of maize resulted in the isolation of more than 50 different genes whose expression is up- or down-regulated after in vitro fertilization (IVF). Among these genes, we identified a **cDNA** encoding the eukaryotic translation initiation factor eIF-5A. This highly conserved factor is thought to be necessary for selective **mRNA** stabilization and translation. It is also the only known protein that contains the unusual amino acid hypusine which is required for biological activity. High **transcript** amounts are stored in the egg cell, which is, in terms of metabolism, relatively inactive. Upon fertilization **transcript** amounts decrease, in contrast to metabolically inactive embryos in which the **transcript cannot** be detected and **transcript** levels increase upon germination. The **expression pattern** during the first embryonic cell cycle is also different from that observed during the somatic cell cycle: egg cells in the G0 phase contain high **transcript** levels, while arrested suspension cells contain few **transcripts**. In the somatic cell cycle, eif-5A is strongly induced during the G1 phase and **transcripts** are continuously degraded during the S, G2 and M phases until new induction during the G1 phase of the next cycle. eif-5A, a member of a small gene family in maize, is expressed in most maize tissues investigated. Based on our results, we suggest that the unfertilized egg cell of maize, although relatively inactive regarding its metabolism, is prepared for selective **mRNA** translation that is quickly triggered after fertilization. We also suggest that the regulation of eif-5A in the first embryonic cell cycle is different from the somatic cell cycle.

L11 ANSWER 21 OF 51 MEDLINE DUPLICATE 14

ACCESSION NUMBER: 1999146420 MEDLINE
DOCUMENT NUMBER: 99146420 PubMed ID: 10023815
TITLE: Tectorin mRNA expression is spatially and temporally restricted during mouse inner ear development.
AUTHOR: Rau A; Legan P K; Richardson G P
CORPORATE SOURCE: School of Biological Sciences, University of Sussex, Falmer, Brighton, United Kingdom.
SOURCE: JOURNAL OF COMPARATIVE NEUROLOGY, (1999 Mar 8) 405 (2) 271-80.
Journal code: 0406041. ISSN: 0021-9967.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199904
ENTRY DATE: Entered STN: 19990504
Last Updated on STN: 19990504
Entered Medline: 19990422

AB The tectorial and otolithic membranes are extracellular matrices that cover the sensory epithelia of the inner ear. They are required for mechanotransduction and may influence hair-cell development. The **mRNA expression patterns** for two major glycoproteins of these matrices, alpha- and beta-tectorin, were examined during mouse inner ear development to determine when and where these proteins are produced relative to hair cells and whether tectorin production is continuous or transient. Using in situ hybridisation, alpha- and beta-tectorin **mRNAs** are first detected in the basal end of the cochlea at embryonic day (E) 12.5, and the distinct patterns observed for each tectorin **mRNA** in the neonate become visible by E14.5. The neonatal **expression patterns** indicate that some cell types in the cochlea express both alpha- and beta-tectorin **mRNAs**, while other cells only express one tectorin **mRNA**. Although expressed early in development, alpha- and beta-tectorin **mRNAs cannot** be detected in the cochlea by postnatal day (P) 22. In the saccule and utricle, alpha-tectorin **mRNA** is detected at E12.5, but beta-tectorin **mRNA** is not observed until E14.5. Expression of alpha-tectorin **mRNA** ceases after P15, whereas beta-tectorin **mRNA** expression continues within the striolar region of the utricle until at least P150. The results show alpha- and beta-tectorin **mRNAs** are expressed during the early stages of inner ear development, prior to or concomitant with hair-cell differentiation, and before the appearance of hair bundles. The **expression patterns** suggest different cell types contribute to the formation of the various regions of the tectorial membrane. Although tectorin **mRNAs** are only expressed transiently during cochlear development, beta-tectorin **mRNA** is continuously expressed within the striolar region of the utricle.

L11 ANSWER 22 OF 51 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 1999137104 MEDLINE
DOCUMENT NUMBER: 99137104 PubMed ID: 9972819
TITLE: Post-transcriptional regulation of the peripheral myelin protein gene PMP22/gas3.
AUTHOR: Bosse F; Brodbeck J; Muller H W
CORPORATE SOURCE: Department of Neurology, Heinrich-Heine-University of Dusseldorf, Federal Republic of Germany.. bosse@uni-duesseldorf.de
SOURCE: JOURNAL OF NEUROSCIENCE RESEARCH, (1999 Jan 15) 55 (2) 164-77.
Journal code: 7600111. ISSN: 0360-4012.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ000642; GENBANK-AJ001035; GENBANK-AJ001036
ENTRY MONTH: 199904
ENTRY DATE: Entered STN: 19990504
Last Updated on STN: 19990504
Entered Medline: 19990420

AB The peripheral myelin protein PMP22 gene has been described as a growth arrest-specific gene gas3 and has been identified as disease gene of various demyelinating neuropathies. The gene consists of two highly conserved alternative noncoding 5'-exons 1a (CD25) and 1b (SR13), respectively. Differential **expression patterns** of these **transcripts** in vivo and in vitro suggest a very complex mode of PMP22 gene regulation, which **cannot** be explained merely by transcriptional control. In fact, the PMP22 gene is regulated on different post-transcriptional levels. While reverse transcriptase polymerase chain reaction (RT-PCR) analyses revealed no alterations in stability for both PMP22 **transcripts** in randomly growing Schwann cell cultures of rat sciatic nerve for at least 8 hours, in serum-induced synchronized cultures of resting cells we observed a specific cell cycle-regulated degradation of both **transcripts**. We further prepared diverse PMP22/CAT fusion genes to study the influence of the alternative 5'UTRs on PMP22 translation. Transient transfection of NIH3T3-fibroblasts and rat Schwann cells demonstrated that the alternative 5'UTRs (CD25 and SR13) and the 3'UTR exert differential regulatory influences on the translation efficiency.

L11 ANSWER 23 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:221876 BIOSIS
DOCUMENT NUMBER: PREV199900221876
TITLE: Expression of basic fibroblast growth factor in squamous cell carcinomas of the larynx - Examination by in situ hybridization.
AUTHOR(S): Quint, C. (1); Neuchrist, C.; Breitschopf, H.; Pammer, J.; Burian, M.
CORPORATE SOURCE: (1) HNO-Universitaetsklinik, Waehringer Guertel 18-20, A-1090, Wien Austria
SOURCE: Onkologie, (Feb., 1999) Vol. 22, No. 1, pp. 41-46.
ISSN: 0378-584X.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English; German

AB Background: Basic fibroblast growth factor (bFGF) is one out of a group of angiogenic factors that are made responsible for the formation of new tumor vessels. The purpose of this study was to show the **expression pattern** of bFGF in squamous cell carcinomas (SCC) of the larynx. Patients and Methods: Specimens of 26 patients with SCC of the larynx were stained for bFGF **transcripts** by in situ hybridization and immunohistochemistry. All patients were treated surgically between 1987 and 1996. Microvessel density was examined immunohistochemically by staining the surface antigen CD34. Results: bFGF **mRNA** expression in tumor cells was either strong (35%), moderate (38%), weak (19%) or undetectable (8%). The connective tissue showed no or only sparse expression of bFGF **transcripts**. Normal mucosa exhibited a more intense staining pattern at basal cell layers, and the intensity varied from weak to moderate. In most of the tumors a varying

staining of macrophages and endothelial cells occurred. Even if tumor cells showed weaker labeling, the staining pattern in immunohistochemical experiments was roughly comparable with the expression of bFGF **mRNA**. Tumor size, lymph node status, histologic differentiation and microvessel density showed no correlation with the intensity of bFGF expression. Conclusions: The main source of bFGF in laryngeal cancer seems to originate from tumor cells. As there is no correlation of bFGF **mRNA** with clinicopathological parameters, other mechanisms such as varying bioavailability by binding of bFGF to a binding protein and production of other angiogenic factors like vascular endothelial growth factor (VEGF) could be involved in the actual effects of bFGF on tumor behavior. Thus, in our hands bFGF **cannot** be addressed as a prognostic marker in laryngeal carcinomas.

L11 ANSWER 24 OF 51 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 1999171392 MEDLINE
DOCUMENT NUMBER: 99171392 PubMed ID: 10073384
TITLE: Expression of the myristoylated alanine-rich C kinase substrate (MARCKS) and MARCKS-related protein (MRP) in the prefrontal cortex and hippocampus of suicide victims.
AUTHOR: McNamara R K; Hyde T M; Kleinman J E; Lenox R H
CORPORATE SOURCE: Department of Psychiatry, University of Pennsylvania School of Medicine, Abramson Research Center, Philadelphia 19104, USA.
SOURCE: JOURNAL OF CLINICAL PSYCHIATRY, (1999) 60 Suppl 2 21-6; discussion 40-1, 113-6.
Journal code: 7801243. ISSN: 0160-6689.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 19990326
Entered Medline: 19990318

AB BACKGROUND: Although suicide is a leading cause of death in the United States and represents a significant public health threat, little is known about the neurobiological or molecular factors that contribute to its pathophysiology. A number of studies now indicate that lithium has considerable efficacy in the prevention of suicide in patients with affective disorders, and accumulating evidence indicates that protein kinase C (PKC) and its substrates, in particular the myristoylated alanine-rich C kinase substrate (MARCKS), are primary targets of chronic lithium treatment. We therefore hypothesized that a dysregulation in MARCKS expression in key brain regions could contribute to the pathophysiology associated with suicide. To address this, we examined MARCKS, as well as the closely related MARCKS-related protein (MRP), **mRNA** expression in the hippocampus and dorsolateral prefrontal cortex of suicide victims and normal controls. METHOD: MARCKS and MRP **mRNA** expression was assessed by quantitative in situ hybridization histochemistry performed on postmortem hippocampal and dorsolateral prefrontal cortex sections from suicide (N = 9) and normal control (N = 10) brains. RESULTS: In the normal hippocampus, both MARCKS and MRP **mRNA** expression were highest in the granule cell layer and low-moderate in CA1, CA3, and hilus. A high level of MRP **mRNA** expression was also observed in the white matter of the fimbria/fornix. Neither MARCKS nor MRP **mRNA** expression levels differed significantly in the granule cell layer, CA3, hilus, or CA1 in suicide victims relative to normal controls (1-way ANOVA, $p > .05$). In the normal

prefrontal cortex, MARCKS was expressed exclusively in gray matter (layers I-VI), whereas MRP was expressed in both gray and white matter. Neither MARCKS nor MRP **mRNA** expression levels in the gray and white matter regions of the dorsal prefrontal cortex differed between suicides and normal controls (1-way ANOVA, p > .05). CONCLUSION: The present findings are the first to demonstrate the expression and distribution of MARCKS and MRP in the human hippocampus and dorsolateral prefrontal cortex, and their **expression pattern** within these regions bears strong resemblance to those observed in the adult rat brain.

Comparison of MARCKS and MRP **mRNA** expression in the hippocampus and prefrontal cortex of suicide victims and normal controls indicates that these 2 **mRNAs** are not differentially regulated in these regions. However, differences in MARCKS and MRP protein expression and function **cannot** be ruled out by the present findings.

L11 ANSWER 25 OF 51 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 1999430855 MEDLINE
DOCUMENT NUMBER: 99430855 PubMed ID: 10503530
TITLE: Genetic mapping and functional analysis of a nodulation-defective mutant (sym19) of pea (Pisum sativum L.).
AUTHOR: Schneider A; Walker S A; Poyser S; Sagan M; Ellis T H; Downie J A
CORPORATE SOURCE: John Innes Centre, Norwich Research Park, Colney, UK.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1999 Aug) 262 (1) 1-11. Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991101
Last Updated on STN: 19991101
Entered Medline: 19991018

AB The pea mutant line P55 is defective in root nodule formation, and this phenotype is controlled by a single recessive gene. Complementation analysis revealed that the mutation in P55 is allelic to sym19, which has previously been mapped to linkage group I. Detailed mapping revealed that the sym19 and ENOD40 loci are separated by 2.7 cM. We identified four recombination events, demonstrating that the nodulation defect caused by mutation of the sym19 locus **cannot** be due to mutation of ENOD40. RT-PCR experiments showed that P55 expresses ENOD12A, but there was little or no increase in the level of its **transcript** in response to Nod factor or infection with Rhizobium. To investigate this **expression pattern** further, transgenic peas carrying a pENOD12A-GUS reporter construct were made. One transgenic line was crossed with line P55, to generate F2 progeny homozygous for sym19 and carrying pENOD12A-GUS. In both WT and sym19 mutant lines, ENOD12A-GUS expression was induced at sites of lateral root emergence in uninoculated plants. In Nod+ plants pENOD12A-GUS was induced in response to Rhizobium leguminosarumn bv. viciae, but no such induction was seen in the Nod- (sym19) mutants.

L11 ANSWER 26 OF 51 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 1998402558 MEDLINE
DOCUMENT NUMBER: 98402558 PubMed ID: 9730988
TITLE: Common and variant properties of intermediate filament proteins from lower chordates and vertebrates; two proteins

from the tunicate Styela and the identification of a type III homologue.
AUTHOR: Riemer D; Weber K
CORPORATE SOURCE: Max Planck Institute for Biophysical Chemistry, Department of Biochemistry, Am Fassberg 11, D-37077 Goettingen, Germany.
SOURCE: JOURNAL OF CELL SCIENCE, (1998 Oct) 111 (Pt 19) 2967-75.

Journal code: 0052457. ISSN: 0021-9533.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ005020; GENBANK-AJ005021
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981230

AB The chordates combine the vertebrates and the invertebrate phyla of the cephalo- and urochordates (tunicates). Two cytoplasmic intermediate filament (IF) proteins of the urochordate Styela plicata are characterized by **cDNA** cloning, gene organization, tissue specific **expression patterns** in the adult animal and the self assembly properties of the recombinant proteins. In line with metazoan phylogeny St-A and St-B have the short length version of the coil 1b domain found in all vertebrate and cephalochordate IF proteins while protostomic IF proteins have the longer length version with an extra 42 residues. St-A is the first IF protein from a lower chordate which can be unambiguously related to a particular vertebrate IF subfamily. St-A shares 46% sequence identity with desmin, displays the N-terminal motif necessary for filament assembly of type III proteins and forms normal homopolymeric 10 nm filaments in vitro. St-A but not St-B is present in smooth muscle cells of the body wall musculature. St-A and St-B are found as separate networks in some interior epithelia. St-B shares 30 to 35% identity with keratin 8, St-A and desmin and does not form IF under in vitro assembly conditions. Its relation to a particular vertebrate IF type or to the eight currently known IF proteins from the cephalochordate Branchiostoma remains unresolved. The striking relation between St-A and desmin predicts that the common progenitor of the urochordate (tunicate) and the cephalochordate/vertebrate lineages already possessed a type III homologue. Unlike in vertebrates intron patterns **cannot** be used to classify the tunicate IF genes. Although St-A is a type III homologue its gene shows an intron position which in vertebrates is restricted to keratin type II genes.

L11 ANSWER 27 OF 51 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 1998318453 MEDLINE
DOCUMENT NUMBER: 98318453 PubMed ID: 9611151
TITLE: Thyroid receptor plasticity in striated muscle types: effects of altered thyroid state.
AUTHOR: Haddad F; Qin A X; McCue S A; Baldwin K M
CORPORATE SOURCE: Department of Physiology and Biophysics, University of California, Irvine, California 92697, USA.
CONTRACT NUMBER: AR-30346 (NIAMS)
HL-38819 (NHLBI)
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1998 Jun) 274 (6 Pt 1) E1018-26.

Journal code: 0370511. ISSN: 0002-9513.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980817
Last Updated on STN: 20020124
Entered Medline: 19980806

AB This study examined nuclear thyroid receptor (TR) maximum binding capacity (Bmax), dissociation constant (Kd), and TR isoform (alpha1, alpha2, beta1) **mRNA** expression in rodent cardiac, "fast-twitch white," "fast-twitch red," and "slow-twitch red" muscle types as a function of thyroid state. These analyses were performed in the context of slow-twitch type I myosin heavy-chain (MHC) expression, a 3,5,3'-triiodothyronine (T3)-regulated gene that displays varying responsiveness to T3 in the above tissues. Nuclear T3 binding analyses show that the skeletal muscle types express more TRs per unit DNA than cardiac muscle, whereas the latter has a lower Kd than the former. Altered thyroid state had little effect on either cardiac Bmax or Kd, whereas hypothyroidism increased Bmax in the skeletal muscle types without affecting its Kd. Cardiac muscle demonstrated the greatest **mRNA** signal of TR-beta1 compared with the other muscle types, whereas the TR-alpha1 **mRNA** signals were more abundant in the skeletal muscle types, especially fast-twitch red. Hyperthyroidism increased the ratio of beta1 to alpha1 and decreased the ratio of alpha2- to alpha1+beta1-**mRNA** signal across the muscle types, whereas hypothyroidism caused the opposite effects. The nuclear T3 affinity correlated significantly with the TR-beta1 **mRNA** expression but not with TR-alpha1 **mRNA** expression. Collectively, these findings suggest that, despite a divergent pattern of TR **mRNA** expression in the different muscle types, these patterns follow similar qualitative changes under altered thyroid state. Furthermore, TR **expression pattern cannot** account for the quantitative and qualitative changes in type I MHC expression that occur in the different muscle types.

L11 ANSWER 28 OF 51 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 1998176640 MEDLINE
DOCUMENT NUMBER: 98176640 PubMed ID: 9517463
TITLE: Learning deficit in BDNF mutant mice.
AUTHOR: Linnarsson S; Bjorklund A; Ernfors P
CORPORATE SOURCE: Department of Molecular Neurobiology, Karolinska Institute, Stockholm, Sweden.
SOURCE: EUROPEAN JOURNAL OF NEUROSCIENCE, (1997 Dec) 9 (12) 2581-7.
Journal code: 8918110. ISSN: 0953-816X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980507
Last Updated on STN: 19980507
Entered Medline: 19980424

AB Brain-derived neurotrophic factor (BDNF) has been implicated in the regulation of high-frequency synaptic transmission and long-term

potentiation in the hippocampus, processes that are also thought to be involved in the learning of spatial tasks such as the Morris water maze. In order to determine whether BDNF is required for normal spatial learning, mice carrying a deletion in one copy of the BDNF gene were subjected to the Morris water maze task. Young adult BDNF mutant mice were significantly impaired compared with wild-type mice, requiring twice the number of days to reach full performance. Aged wild-type mice performed significantly worse than young wild-type mice and the effect was even more pronounced in the BDNF mutant mice, which did not learn at all. Although there was no difference in mean swimming speed between BDNF mutant and wild-type mice, we **cannot** exclude the possibility that developmental or peripheral deficits also contribute to the learning deficits in these mice. In situ hybridization and RNase protection analysis revealed that BDNF **mRNA** expression was indeed decreased in BDNF mutant mice. Furthermore, a pronounced effect of age on BDNF **mRNA** expression was seen, displayed as both a reduced level of **mRNA** expression and a reduced or entirely absent layer-specific **expression pattern** in the cerebral cortex of aged animals. Thus, our data suggest that BDNF expression may be linked to learning.

L11 ANSWER 29 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1997:458413 BIOSIS
DOCUMENT NUMBER: PREV199799757616
TITLE: Regional expression and cellular localization of the alpha-1 and beta subunit of high voltage-activated calcium channels in rat brain.
AUTHOR(S): Ludwig, Andreas (1); Flockerzi, Veit; Hofmann, Franz
CORPORATE SOURCE: (1) Inst. Pharmakol. Toxikol., Technische Univ. Muenchen, Biedersteiner Str. 29, 80802 Muenchen Germany
SOURCE: Journal of Neuroscience, (1997) Vol. 17, No. 4, pp. 1339-1349.
ISSN: 0270-6474.
DOCUMENT TYPE: Article
LANGUAGE: English

AB The neuronal high voltage-activated calcium channels are a family of ion channels composed from up to five different a, and four different beta subunits. The neuronal distribution and subunit composition of calcium channels were investigated using subunit-specific antibodies and riboprobes. The beta subunit-specific antibodies identified the presence of beta-1a in skeletal muscle; beta-2 in heart; and beta-2, beta-3, and beta-4 in brain. The beta-3 protein was widely distributed in rat brain, with prominent labeling of olfactory bulb, cortex, hippocampus, and habenula. The beta-4 protein was also widely expressed, most prominently in the cerebellum. beta-2 protein was expressed at only low levels. In situ hybridization with beta subunit-specific riboprobes confirmed the differential **expression pattern** of the individual subunits. Hybridization with riboprobes specific for the alpha-1A, alpha-1B, alpha-1C, and alpha-1D subunits showed a broad distribution of alpha-1A, and alpha-1B **transcripts**, whereas the expression level of alpha-1C and alpha-1D **mRNA** was lower and more spatially restricted. The overall **expression pattern** and cellular localization suggested that beta-4 may associate predominantly, but probably not exclusively, with the alpha-1A subunit, and beta-3 with the alpha-1B subunit. In certain brain areas such as the habenula, the beta-3 subunit may associate with other alpha-1 subunits too. Furthermore, the beta-2 subunit may form complexes with different alpha-1 subunits in brain and cardiac muscle. These results demonstrate that a given beta

subunit may associate with different alpha-1 subunits in a cell type-dependent manner, contributing to the diversity of the neuronal calcium channels. at wild-type levels in the mutant granule cells, indicating a post-translational loss of the delta subunit. These results provide genetic evidence for a specific association between the alpha-6 and delta subunits. Because in alpha-6 -/- neurons the remaining alpha-1, beta-2/3, and gamma-2 subunits **cannot** rescue the delta subunit, certain potential subunit combinations may not be found in wild-type cells.

L11 ANSWER 30 OF 51 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 1998012524 MEDLINE
DOCUMENT NUMBER: 98012524 PubMed ID: 9351239
TITLE: Conserved expression of a TASSELSEED2 homolog in the tapetum of the dioecious Silene latifolia and Arabidopsis thaliana.
AUTHOR: Lebel-Hardenack S; Ye D; Koutnikova H; Saedler H; Grant S R
CORPORATE SOURCE: Max-Planck-Institute for Plant Breeding, Cologne, Germany.
SOURCE: PLANT JOURNAL, (1997 Sep) 12 (3) 515-26.
Journal code: 9207397. ISSN: 0960-7412.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U76501
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980116
Last Updated on STN: 19990129
Entered Medline: 19971224
AB To investigate the genetics of male sex determination and stamen development in the dioecious plant Silene latifolia (white campion), male-specific **transcripts** were isolated from developing flowers by **cDNA** subtraction. One of the **cDNAs** identified, STA1, had high DNA and amino acid sequence homology to the male sex determining gene of Zea mays (maize), TASSELSEED2. Both genes are expressed in male and not in female flowers, However, they do not share the same **expression pattern**. The TASSELSEED2 gene product is expressed in the gynoecium primordia of male maize flowers where it is necessary for pistil abortion. STA1 is not expressed in the gynoecium primordia of male white campion and therefore its gene product **cannot** perform the same function in sex determination that TASSELSEED2 performs in maize. STA1 is expressed in tapetal cells of white campion male flowers and of white campion hermaphroditic mutants. A homologous gene is also expressed in the tapetum of hermaphroditic Silene species. Tapetal expression of a homologous gene (named ATA1) was also found in Arabidopsis thaliana. The similarity in primary sequence and **expression pattern** of STA1 and ATA1 indicate that these genes have a conserved role in tapetum development.

L11 ANSWER 31 OF 51 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 96400033 MEDLINE
DOCUMENT NUMBER: 96400033 PubMed ID: 8806409
TITLE: Isolation of an additional soybean cDNA encoding Ypt/Rab-related small GTP-binding protein and its functional comparison to Sypt using a yeast ypt1-1 mutant.
AUTHOR: Kim W Y; Cheong N E; Lee D C; Lee K O; Je D Y; Bahk J D; Cho M J; Lee S Y

CORPORATE SOURCE: Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Chinju, Korea.
SOURCE: PLANT MOLECULAR BIOLOGY, (1996 Jul) 31 (4) 783-92.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U32185; SWISSPROT-UNKNOWN
ENTRY MONTH: 199611
ENTRY DATE: Entered STN: 19961219
Last Updated on STN: 20000303
Entered Medline: 19961101

AB We have previously reported the isolation of a gene from a soybean **cDNA** library encoding a Ypt/Rab-related small GTP-binding protein, Sypt. Here, we report the isolation of a second Ypt/Rab-related gene, designated Srab2, from the same soybean **cDNA** library. And we compare the in vivo function of the two soybean genes utilizing a yeast ypt1-1 mutant. The Srab2 gene encodes 211 amino acid residues with a molecular mass of 23 169 Da. The deduced amino acid sequence of the Srab2 is closely related to the rat (76%) and human (75%) Rab2 proteins, but it shares relatively little homology to Sypt (46%) and Saccharomyces cerevisiae ypt proteins (41%). Genomic Southern blot analysis using the **cDNA** insert of Srab2 revealed that it belongs to a multigene family in the soybean genome. The protein encoded by Srab2 gene, when expressed in Escherichia coli, disclosed a GTP-binding activity. The **expression pattern** of the Srab2 gene is quite different from that of the Sypt gene. The Srab2 gene is predominantly expressed in the plumule region, while expression was very low in the other areas in soybean seedlings. On the other hand, the Sypt **mRNA** is not detectable in any tissues of soybean seedlings grown in the dark. However, light significantly suppressed the Srab2 gene expression, but enhanced the **transcript** levels of the Sypt gene in leaf and, at even higher levels, in root tissues. When the Srab2 and Sypt genes are introduced separately into a S cerevisiae defective in vesicular transport function, the Srab2 gene **cannot** complement the temperature-sensitive yeast ypt1-1 mutation at all, in contrast to the Sypt gene. In conclusion, the difference of functional complementation of the yeast mutation together with differential expression of the two genes suggest that the in vivo roles of the Srab2 and Sypt genes may be different in soybean cells.

L11 ANSWER 32 OF 51 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 97048719 MEDLINE
DOCUMENT NUMBER: 97048719 PubMed ID: 8893550
TITLE: Fluorescent imaging of GUS activity and RT-PCR analysis of gene expression in the shoot apical meristem.
AUTHOR: Fleming A J; Manzara T; Gruissem W; Kuhlemeier C
CORPORATE SOURCE: Institute of Plant Physiology, University of Berne, Switzerland.
SOURCE: PLANT JOURNAL, (1996 Oct) 10 (4) 745-54.
Journal code: 9207397. ISSN: 0960-7412.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19980206
Entered Medline: 19970123

AB The use of promoter-reporter gene constructs in transgenic plants is a powerful tool in the analysis of gene expression which can, however, be limited in the resolution of small structures, such as the apical meristem. This paper reports on a fluorescent imaging technique for the analysis of GUS reporter gene expression to cellular resolution in the apical meristem of tomato. Using this technique in combination with an RT-PCR analysis of RBS gene-specific **transcript** levels, it is shown that: 5' upstream sequences of RBCS genes are sufficient to mimic the pattern of **transcripts** revealed by in situ hybridisation (no expression in the apical meristem, high expression in the initiated leaf primordia); the genes RBCS2, RBCS3A and RBCS3B are transcriptionally activated upon primordium initiation with **transcripts** for RBCS1 and RBCS3C accumulating later in leaf development; and that RBCS promoter activity **cannot** be induced in the apical meristem by light, an environmental signal which elevates RBCS **transcript** level in other aerial parts of the plant. These data provide a detailed picture of the complex transcriptional events occurring on leaf initiation and the establishment of the photosynthetic machinery; they describe two complementary techniques which allow the analysis of such complex events at the tissue and cellular level; and they characterize an in vivo assay system which can be used to analyse the factors involved in the initiation and maintenance of gene **expression patterns** in the apical meristem.

L11 ANSWER 33 OF 51 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 96400454 MEDLINE
DOCUMENT NUMBER: 96400454 PubMed ID: 8806830
TITLE: The enzymatic activity of Drosophila AWD/NDP kinase is necessary but not sufficient for its biological function.
AUTHOR: Xu J; Liu L Z; Deng X F; Timmons L; Hersperger E; Steeg P S; Veron M; Shearn A
CORPORATE SOURCE: Department of Biology, Johns Hopkins University, Baltimore, Maryland 21218, USA.
SOURCE: DEVELOPMENTAL BIOLOGY, (1996 Aug 1) 177 (2) 544-57. Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199610
ENTRY DATE: Entered STN: 19961106
Last Updated on STN: 19961106
Entered Medline: 19961024

AB The Drosophila abnormal wing discs (awd) gene encodes the subunit of a protein that has nucleoside diphosphate kinase (NDP kinase) activity. Null mutations of the awd gene cause lethality after puparium formation. Larvae homozygous for such mutations have small imaginal discs, lymph glands, and brain lobes. Neither the imaginal discs nor the ovaries from such null mutant larvae are capable of further growth or normal differentiation when transplanted into suitable host larvae. This null mutant phenotype can be entirely rescued by one copy of a transgene that has 750 bp of awd upstream regulatory DNA fused to a full-length awd **cDNA**. Tissue-specific expression of AWD protein from this rescue transgene is identical to tissue-specific expression of beta-galactosidase from a reporter transgene that has the same regulatory region fused to the

bacterial lac Z gene. However, this rescue transgene or reporter transgene
expression pattern is only a subset of the endogenous pattern of expression detected by either in situ hybridization or immunohistochemistry. This suggests that awd is normally expressed in some
tissues where it is not required. The null mutant phenotype **cannot** be rescued at all by a transgene that has 750 bp of awd upstream regulatory DNA fused to a full-length awd **cDNA** with a mutation that eliminates NDP kinase activity by replacement of the active site histidine with alanine. This suggests that the enzymatic activity of the AWD protein is necessary for its biological function. The human genes nm23-H1 and nm23-H2 encode NDP kinase A and B subunits, respectively. The protein subunit encoded by either human nm23 gene is 78% identical to that
encoded by the Drosophila awd gene. Transgenes that have the 750-bp awd upstream regulatory DNA fused to human nm23-H2 **cDNA** but not to nm23-H1 **cDNA** can rescue the imaginal disc phenotype and the zygotic lethality caused by homozygosis for an awd null mutation as efficiently as an awd transgene. However, rescue of female sterility requires twice as much nm23-H2 expression as awd expression. This implies that the enzymatic activity of the AWD protein is not sufficient for its biological function. The biological function may require nonconserved residues of the AWD protein that allow it to interact with other proteins.

L11 ANSWER 34 OF 51 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 97026122 MEDLINE
DOCUMENT NUMBER: 97026122 PubMed ID: 8872301
TITLE: Distinctions between hippocampus of mouse and rat: protein F1/GAP-43 gene expression, promoter activity, and spatial memory.
AUTHOR: McNamara R K; Namgung U; Routtenberg A
CORPORATE SOURCE: Cresap Neuroscience Laboratory, Department of Psychology, Northwestern University, Evanston, IL 60208 USA.
CONTRACT NUMBER: MH25281-21 (NIMH)
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (1996 Sep 1) 40 (2) 177-87.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19980206
Entered Medline: 19970115

AB We began these experiments as an attempt to replicate in the mouse the induction by kainate (KA) of F1/GAP-43 **mRNA** we observed in adult rat hippocampal granule cells [Mol. Brain Res., 33 (1995) 22-28]. However,
even though KA induced behavioral seizures in the mouse similar to those in the rat, neither induction of F1/GAP-43 **mRNA** nor subsequent mossy fiber sprouting observed in the rat was detected in three different mouse strains. It was also surprising that the distribution of constitutive levels of F1/GAP-43 **mRNA** in mouse and rat hippocampus was qualitatively different. Indeed, F1/GAP-43 expression in CA3 pyramidal cells was significantly greater in rat than mouse, while F1/GAP-43 expression in CA1 cells of rat and mouse was equivalent using densitometric analysis. Thus, F1/GAP-43 expression in rat is quantitatively higher in CA3 and CA1 pyramidal cells. In mouse, expression

was equivalent in these two subfields. In a transgenic mouse bearing a rat F1/GAP-43 promoter-reporter (lacZ) construct (line 252), in-vivo promoter activity of F1/GAP-43 was studied in hippocampal cells. Transgene expression in hippocampal pyramidal subfields, high in CA3, low in CA1 pyramidal cells, paralleled the distribution of rat F1/GAP-43 **mRNA** levels, not mouse. Differences in the constitutive F1/GAP-43 **expression pattern** in hippocampus between rat and mouse may therefore be determined by different recognition elements present on the F1/GAP-43 promoter. KA injected into the line 252 transgenic mouse did not activate the rat F1/GAP-43 promoter in mouse hippocampal granule cells. The absence of both F1/GAP-43 **mRNA** expression induction and promoter activation in mouse granule cells after KA is likely related to genera differences in transcriptional regulatory mechanisms, though post-transcriptional mechanisms **cannot** be excluded. Since the different hippocampal chemistry of F1/GAP-43 in rat and mouse likely extends to other molecular species, behaviors in rat and mouse that depend on hippocampal function might be different as well. We therefore evaluated spatial memory ability in a delayed matching-to-sample task. In contrast to rat, we were surprised to find no evidence of the ability to learn this task in three different mouse strains. Since interest in mouse genetics in relation to behavior and memory functions of hippocampus is growing, generalizations concerning hippocampal function from studies carried out on the mouse need to be made with caution considering the specific behavioral, pharmacological, and general molecular differences observed here. One can also be opportunistic and exploit the natural variations between these two genera to gain insight into the molecular mechanisms underlying information storage.

L11 ANSWER 35 OF 51 MEDLINE DUPLICATE 26
ACCESSION NUMBER: 96180988 MEDLINE
DOCUMENT NUMBER: 96180988 PubMed ID: 8605252
TITLE: Regulation of differential expression of platelet-derived growth factor alpha- and beta-receptor mRNA in normal and malignant human mesothelial cell lines.
AUTHOR: Langerak A W; van der Linden-van Beurden C A; Versnel M A
CORPORATE SOURCE: Department of Immunology, Erasmus University, Rotterdam, The Netherlands.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1996 Feb 7) 1305 (1-2) 63-70.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199605
ENTRY DATE: Entered STN: 19960531
Last Updated on STN: 20000303
Entered Medline: 19960523

AB In earlier studies we showed that the expression of patterns of platelet-derived growth factor (PDGF) alpha- and beta-receptors differ between normal and malignant mesothelial cell lines. Normal mesothelial cells predominantly express PDGF alpha-receptor **mRNA** and protein, whereas most malignant mesothelioma cell lines produce PDGF beta-receptor **mRNA** and protein. In this paper we studied regulation of this differential PDGF receptor **mRNA** expression.

Such an analysis is of importance in view of the suggested PDGF autocrine activity involving the PDGF beta-receptor mesothelioma cells. The results obtained in this study demonstrate that malignant mesothelioma cell lines are not only capable of PDGF beta-receptor transcription but of alpha-receptor transcription as well, as evidenced from run off analysis and RT-PCR using alpha-receptor specific primers. However, the fact that PDGF alpha-receptor **mRNA** could not be detected by Northern blot analysis, even after cycloheximide treatment, suggests a difference in steady-state PDGF alpha-receptor **mRNA** expression levels between normal and malignant mesothelial cell lines, which is likely to be caused by a post-transcriptional mechanism. In normal mesothelial cells a half-life of more than 6 h was observed for PDGF alpha-receptor **mRNA**. In the majority of malignant mesothelioma cell lines clear PDGF beta-receptor **mRNA** expression was seen. The half-life of the PDGF beta-receptor **transcript** was at least 6 h in these cells. In contrast, hardly any PDGF beta-receptor transcription was observed in run off assays in normal mesothelial cells, suggesting that differences in beta-receptor transcriptional initiation most probably account for the inability to clearly detect PDGF beta-receptor **transcripts** in these cells. Transforming growth factor beta-1 (TGF-beta 1), which is being produced in active form by mesothelial cells was evaluated for its potential role in regulation of the differential PDGF receptor expression in these cells. Stimulation with TGF-beta 1 revealed decreased PDGF alpha-receptor **mRNA** expression in normal mesothelial cells. The effect on PDGF beta-receptor **mRNA** in the malignant mesothelioma cell lines was variable. Although the TGF-beta 1 effect **cannot** entirely explain the differential PDGF receptor **expression pattern**, TGF-beta 1 may nevertheless play a role in downregulation of an (already) low PDGF alpha-receptor **mRNA** level in malignant mesothelioma cell lines.

L11 ANSWER 36 OF 51 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 95348228 MEDLINE
DOCUMENT NUMBER: 95348228 PubMed ID: 7622596
TITLE: Molecular genetic analysis of myoC, a Dictyostelium myosin I.
AUTHOR: Peterson M D; Novak K D; Reedy M C; Ruman J I; Titus M A
CORPORATE SOURCE: Department of Cell Biology, Duke University Medical Center,
Durham, NC 27710, USA.
CONTRACT NUMBER: RO1AR14317-22 (NIAMS)
SOURCE: JOURNAL OF CELL SCIENCE, (1995 Mar) 108 (Pt 3) 1093-103.
Journal code: 0052457. ISSN: 0021-9533.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L35323; GENBANK-X70400
ENTRY MONTH: 199508
ENTRY DATE: Entered STN: 19950911
Last Updated on STN: 19950911
Entered Medline: 19950829

AB The protozoan myosin Is are widely expressed actin-based motors, yet their in vivo roles remain poorly understood. Molecular genetic studies have been carried out to determine their in vivo function in the simple eukaryote Dictyostelium, an organism that contains a family of four myosin Is. Here we report the characterization of myoC, a gene that encodes a fifth member of this family. Analysis of the deduced amino acid sequence

reveals that the myoC gene encodes a myosin that is homologous to the well-described Acanthamoeba myosin Is as well as to Dictyostelium myoB and -D. The **expression pattern** of the myoC **mRNA** is similar to that of myoB and myoD, with a peak of expression at times of maximal cell migration, around 6 hours development. Deletion of the myoB gene has been previously shown to result in mutant cells that are defective in pseudopod extension and phagocytosis. However, no obvious differences in cell growth, development, phagocytosis or motility were detected in cells in which the myoC gene had been disrupted by homologous recombination. F-actin localization and ultrastructural organization also appeared unperturbed in myoC- cells. This apparent 'lack' of phenotype in a myosin I single knockout **cannot** be simply explained by redundancy of function. Our results rather suggest that the present means of assessing myosin I function in vivo are insufficient to identify the unique roles of these actin-based motors.

L11 ANSWER 37 OF 51 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 96010258 MEDLINE
DOCUMENT NUMBER: 96010258 PubMed ID: 7573368
TITLE: Detection of heterogeneous Epstein-Barr virus gene expression patterns within individual post-transplantation lymphoproliferative disorders.
AUTHOR: Oudejans J J; Jiwa M; van den Brule A J; Grasser F A; Horstman A; Vos W; Kluin P M; van der Valk P; Walboomers J M; Meijer C J
CORPORATE SOURCE: Department of Pathology, Free University Hospital, Amsterdam, The Netherlands.
SOURCE: AMERICAN JOURNAL OF PATHOLOGY, (1995 Oct) 147 (4) 923-33.
Journal code: 0370502. ISSN: 0002-9440.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199511
ENTRY DATE: Entered STN: 19951227
Last Updated on STN: 19951227
Entered Medline: 19951109

AB Using RT-PCR analysis of Epstein-Barr virus (EBV) latent gene transcription in EBV-harboring cell lines (JY and RAJI) and in post-transplantation lymphoproliferative disorders (PT-LPDs), we detected transcription of all tested latent genes (EBNA1, EBNA2, LMP1, LMP2A, and BARF0) in all cases, suggesting the presence of similar EBV **expression patterns** in both PT-LPDs and cell lines. In addition, the detection of immediate early (ZEBRA) and early gene (BHRF1) **transcripts** in cell lines and PT-LPDs indicates that activation of the virus lytic cycle occurs. To investigate EBV **expression patterns** at the single-cell level, a combination of immunohistochemistry and RNA in situ hybridization (including double-staining procedures) was used. In the JY and RAJI cell lines, the latency type 3 **expression pattern** was detected in 80 to 90% of the cells as shown by the co-expression of EBNA2 and LMP1. In contrast, in the three PT-LPDs that could be analyzed by double staining, cells expressing both EBNA2 and LMP1 were rarely detected. A mixture of at least three different cell populations were identified: (1) cells exclusively expressing EBER1/2 and EBNA1 (latency type 1); (2) cells expressing EBER1/2, EBNA1, and LMP1 (latency type 2); and (3) cells expressing EBER1/2, EBNA1, and EBNA2 in the absence of LMP1. Activation of

the lytic cycle was observed in a small minority of cells, as demonstrated by detection of ZEBRA and EA-D in all cases and GP350/220 in two cases. Thus, in contrast to EBV-transformed cell lines, the observed EBV gene **expression pattern** in PT-LPDs reflects a mixture of multiple EBV-harboring subpopulations expressing different subsets of EBV-encoded proteins. These data indicate that the operational definitions of EBV latencies in vitro **cannot** easily be applied to PT-LPDs but that a continuum of different latency **expression patterns** can be detected at the single cell level in these lymphomas with, in a small minority of cells, progression to the virus lytic cycle.

L11 ANSWER 38 OF 51 MEDLINE
ACCESSION NUMBER: 96014260 MEDLINE
DOCUMENT NUMBER: 96014260 PubMed ID: 7583149
TITLE: Analysis of gene expression in a complex differentiation hierarchy by global amplification of cDNA from single cells.
COMMENT: Erratum in: Curr Biol 1995 Oct 1;5(10):1201
AUTHOR: Brady G; Billia F; Knox J; Hoang T; Kirsch I R; Voura E B; Hawley R G; Cumming R; Buchwald M; Siminovitch K
CORPORATE SOURCE: Ontario Cancer Institute, Toronto, Canada.
SOURCE: CURRENT BIOLOGY, (1995 Aug 1) 5 (8) 909-22.
Journal code: 9107782. ISSN: 0960-9822.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19980206
Entered Medline: 19951212

AB BACKGROUND: Many differentiating tissues contain progenitor cells that differ in their commitment states but **cannot** be readily distinguished or segregated. Molecular analysis is therefore restricted to mixed populations or cell lines which may also be heterogeneous, and the critical differences in gene expression that might determine divergent development are obscured. In this study, we combined global amplification of **mRNA transcripts** in single cells with identification of the developmental potential of processed cells on the basis of the fates of their sibling cells from clonal starts. RESULTS: We analyzed clones of from four to eight hemopoietic precursor cells which had a variety of differentiative potentials; sibling cells generally each formed clones of identical composition in secondary culture. Globally amplified **cDNA** was prepared from individual precursors whose developmental potential was identified by tracking sibling fates. Further **cDNA** samples were prepared from terminally maturing, homogeneous hemopoietic cell populations. Together, the samples represented 16 positions in the hemopoietic developmental hierarchy. **Expression patterns** in the sample set were determined for 29 genes known to be involved in hemopoietic cell growth, differentiation or function. The **cDNAs** from a bipotent erythroid/megakaryocyte precursor and a bipotent neutrophil/macrophage precursor were subtractively hybridized, yielding numerous differentially expressed **cDNA** clones. Hybridization of such clones to the entire precursor sample set identified **transcripts** with consistent patterns of differential expression in the precursor hierarchy. CONCLUSIONS: Tracking of sibling fates reliably

identifies the differentiative potential of a single cell taken for PCR analysis, and demonstrates the existence of a variety of distinct and stable states of differentiative commitment. Global amplification of **cDNA** from single precursor cells, identified by sibling fates, yields a true representation of lineage- and stage-specific gene expression, as confirmed by hybridization to a broad panel of probes. The results provide the first expression mapping of these genes that distinguishes between progenitors in different commitment states, generate new insights and predictions relevant to mechanism, and introduce a powerful set of tools for unravelling the genetic basis of lineage divergence.

L11 ANSWER 39 OF 51 MEDLINE DUPLICATE 29
ACCESSION NUMBER: 95360003 MEDLINE
DOCUMENT NUMBER: 95360003 PubMed ID: 7633444
TITLE: Structural organization and developmental expression pattern of the mouse WD-repeat gene DMR-N9 immediately upstream of the myotonic dystrophy locus.
AUTHOR: Jansen G; Bachner D; Coerwinkel M; Wormskamp N; Hameister H; Wieringa B
CORPORATE SOURCE: Department of Cell Biology and Histology, Medical Faculty, University of Nijmegen, The Netherlands.
SOURCE: HUMAN MOLECULAR GENETICS, (1995 May) 4 (5) 843-52. Journal code: 9208958. ISSN: 0964-6906.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Z38011; GENBANK-Z38012; GENBANK-Z38013; GENBANK-Z38015
ENTRY MONTH: 199509
ENTRY DATE: Entered STN: 19950921
Last Updated on STN: 20020420
Entered Medline: 19950914

AB The diverse biological consequences of size-expansion of the unstable (CTG)n repeat in the myotonic dystrophy protein kinase (DM-PK) gene at chromosome region 19q13.3, are still poorly understood. Abnormal (CTG)n length may affect either DM-PK **mRNA** fate or function, or alternatively, compromise gene transcription by distortion of chromatin configuration. In the latter model involvement of neighbouring genes in DM upon extreme expansion of the repeat **cannot** be discarded as a possibility and should be studied further. Here we report on the elucidation of the complete genomic structure and **expression pattern** of the mouse DMR-N9 gene (called 59 gene in humans), which is at 1.1 kbp upstream of the DM-PK gene. This gene contains five exons spanning 7 kbp and codes for a protein of 650 amino acids. Two regions of the predicted protein show significant homology to WD repeats, highly conserved amino acid sequences found in a family of proteins engaged in signal transduction or cell regulatory functions. The start site of transcription has been determined and we have identified putative transcription factor binding sequences in a 400 bp putative promoter area immediately upstream of the transcribed unit. Northern blotting analysis and RNA in situ hybridization revealed ubiquitous low expression in all tissues of the mouse embryo and enhanced expression in adult brain and testis. The onset of transcription is phased early in mouse embryogenesis, before or at day 9.5 of gestation. From day 14.5 onwards DMR-N9 **mRNAs** were detected in all neural tissues, especially in the telencephalon and mesencephalon. Later, **mRNA** presence is evident

in distinct tubules of the mature testis, restricted to secondary spermatocytes of stages VIII to XII of the spermatogenic proliferation cycle. We conclude that the DMR-N9 gene is a candidate for being involved in the manifestation of mental and testicular symptoms in severe cases of DM.

L11 ANSWER 40 OF 51 MEDLINE DUPLICATE 30
ACCESSION NUMBER: 95394506 MEDLINE
DOCUMENT NUMBER: 95394506 PubMed ID: 7665217
TITLE: Insulin- and insulin-like growth-factor-I receptor tyrosine-kinase activities in human renal carcinoma.
AUTHOR: Kellerer M; von Eye Corleta H; Muhlhofer A; Capp E; Mosthaf L; Bock S; Petrides P E; Haring H U
CORPORATE SOURCE: Institut fur Diabetesforschung, Munich, Germany.
SOURCE: INTERNATIONAL JOURNAL OF CANCER, (1995 Sep 4) 62 (5) 501-7.
Journal code: 0042124. ISSN: 0020-7136.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199510
ENTRY DATE: Entered STN: 19951020
Last Updated on STN: 20000303
Entered Medline: 19951010

AB We studied expression and functional characteristics of the insulin- and insulin-like-growth-factor-I (IGF-I) receptors in human renal carcinoma. Ligand-binding properties and tyrosine-kinase activity of both receptors, as well as the expression of the 2 isoforms of the human insulin receptor (HIR-A and -B) were analyzed in renal carcinoma and normal adjacent kidney tissue of 8 adult patients. Partially purified insulin- and IGF-I receptors from normal and renal cell carcinoma tissue possessed identical affinities for their ligands. Renal cell carcinoma, however, contained 3- to 4-fold more specific insulin-binding sites and 2-fold more IGF-I binding sites than adjacent normal kidney tissue. In addition, we determined the relative content of insulin/IGF-I receptor hybrids in both tissues. Renal cell carcinoma and adjacent normal tissue revealed similar amounts of insulin/IGF-I receptor hybrids, i.e., 44 +/- 8.2% of tracer IGF-I binding in normal tissue and 46 +/- 12.0% in renal cell carcinoma. When equal amounts of insulin- and IGF-I receptor protein were studied, we found significantly increased receptor autophosphorylation and elevated substrate phosphorylation in carcinoma tissue. To assess whether the differences in insulin-receptor tyrosine-kinase activity were caused by an altered pattern of insulin receptor isoform expression, we determined **mRNA** levels for HIR-A and -B. The 2 insulin receptor isoforms were, however, expressed in highly variable ratios in both normal and tumor tissue. Our experiments show that renal carcinoma expresses an elevated amount of insulin- and IGF-I receptor protein with increased specific autophosphorylation and tyrosine-kinase activity each. The increase of insulin-receptor tyrosine-kinase activity in renal carcinoma **cannot** be explained by an altered **expression pattern** of insulin receptor isoforms.

L11 ANSWER 41 OF 51 MEDLINE DUPLICATE 31
ACCESSION NUMBER: 96096312 MEDLINE
DOCUMENT NUMBER: 96096312 PubMed ID: 7490544
TITLE: Effects of maternal diabetes on fetal expression of

insulin-like growth factor and insulin-like growth factor binding protein mRNAs in the rat.

AUTHOR: Streck R D; Rajaratnam V S; Fishman R B; Webb P J

CORPORATE SOURCE: Division of Reproductive & Developmental Toxicology, Department of Health and Human Services, Jefferson, AR 72079, USA.

SOURCE: JOURNAL OF ENDOCRINOLOGY, (1995 Nov) 147 (2) R5-8. Journal code: 0375363. ISSN: 0022-0795.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199601

ENTRY DATE: Entered STN: 19960125
Last Updated on STN: 19960125
Entered Medline: 19960104

AB Maternal diabetes is associated in humans and rats with an increased risk for fetal growth abnormalities and malformations. Therefore, the effect of maternal diabetes on expression of genes that regulate fetal growth and differentiation is of considerable interest. Developmental growth is regulated in part by the expression and availability of insulin-like growth factors (IGFs). Postnatal expression of a subset of the IGFs and IGF binding proteins (IGFBPs) has been demonstrated to be regulated in response to diabetes and other metabolic conditions. We used in situ hybridization to analyze the effect of maternal diabetes, induced by streptozotocin (STZ) prior to mating, upon prenatal rat IGF and IGFBP **mRNA** expression. At gestational day (GD) 14, the most striking effect of maternal diabetes on fetal IGF/IGFBP gene expression was a marked increase in the abundance of IGFBP-1 **mRNA** within the liver primordia of fetuses isolated from diabetic dams compared to age-matched controls. This upregulation **cannot** be entirely due to the approximately one-half-day delay in fetal development (based on limb bud staging) associated with maternal diabetes, as there was no gross difference in the level of IGFBP-1 **mRNA** between GD13 and GD14 control fetal livers. In contrast, the fetal **mRNA** **expression patterns** of IGF-I, IGF-II and IGFBP-2, -3, -4, -5 and -6 were not grossly altered by maternal diabetes. These data are consistent with the hypothesis that IGFBP-1 produced within the fetal liver and secreted into fetal circulation may play a role in regulating rat fetal growth.

L11 ANSWER 42 OF 51 MEDLINE DUPLICATE 32

ACCESSION NUMBER: 94274047 MEDLINE

DOCUMENT NUMBER: 94274047 PubMed ID: 7911774

TITLE: Functional differences between Ultrabithorax protein isoforms in Drosophila melanogaster: evidence from elimination, substitution and ectopic expression of specific isoforms.

AUTHOR: Subramaniam V; Bomze H M; Lopez A J

CORPORATE SOURCE: Department of Biological Sciences, Carnegie Mellon University, Pittsburgh, Pennsylvania 15213.

CONTRACT NUMBER: RO1 HD28664 (NICHD)

SOURCE: GENETICS, (1994 Mar) 136 (3) 979-91. Journal code: 0374636. ISSN: 0016-6731.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199407

ENTRY DATE: Entered STN: 19940729
Last Updated on STN: 19950206
Entered Medline: 19940715

AB The homeotic selector gene Ultrabithorax (Ubx) specifies regional identities in multiple tissues within the thorax and abdomen of Drosophila melanogaster. Ubx encodes a family of six developmentally specific homeodomain protein isoforms translated from alternatively spliced **mRNAs**. The mutant allele Ubx195 contains a stop codon in exon mII, one of three differential elements, and consequently produces functional UBX protein only from **mRNAs** of type IVa and IVb, which are expressed mainly in the central nervous system. Although it retains activity for other processes, Ubx195 behaves like a null allele with respect to development of the peripheral nervous system, indicating that UBX-IVa and IVb alone do not contribute detectable Ubx function for this tissue. The mutant allele UbxMX17 contains an inversion of exon mII. We find that this allele only produces **mRNAs** of type IVa, but the **expression pattern** of the resulting UBX-IVa protein is indistinguishable from that of total UBX protein expression in wild-type embryos. The phenotype of homozygous UbxMX17 embryos indicates that UBX-IVa **cannot** substitute functionally for other isoforms to promote normal development of the peripheral nervous system. This functional limitation is confirmed by a detailed analysis of the peripheral nervous system in embryos that express specific UBX isoforms ectopically under control of a heat shock promoter. Additional observations suggest that UBX isoforms also differ in their ability to function in other tissues.

L11 ANSWER 43 OF 51 MEDLINE DUPLICATE 33
ACCESSION NUMBER: 95113168 MEDLINE
DOCUMENT NUMBER: 95113168 PubMed ID: 7813770
TITLE: Expression patterns of Hoxb genes in the Xenopus embryo suggest roles in anteroposterior specification of the hindbrain and in dorsoventral patterning of the mesoderm.
AUTHOR: Godsave S; Dekker E J; Holling T; Pannese M; Boncinelli E; Durston A
CORPORATE SOURCE: Netherlands Institute for Developmental Biology, Utrecht.
SOURCE: DEVELOPMENTAL BIOLOGY, (1994 Dec) 166 (2) 465-76.
Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199502
ENTRY DATE: Entered STN: 19950217
Last Updated on STN: 19950217
Entered Medline: 19950209

AB Hox genes are thought to participate in patterning the anteroposterior (a-p) axis during vertebrate embryogenesis. In this investigation, the spatial expression of six Hoxb genes was analyzed in early embryos of Xenopus laevis by in situ hybridization. Hoxb gene expression was first detected in late gastrulae/early neurulae, by which stage, the characteristic spatially colinear Hoxb gene expression sequence was already apparent. Dissection experiments indicated that the establishment of these localized **expression patterns** coincides with the acquisition of anteroposterior positional information along the main body axis. The Hoxb genes continued to be expressed in similar domains along the anteroposterior axis at all developmental stages examined, although there were some changes in expression at the cellular level. Interestingly, the 3' genes, Hoxb-1, Hoxb-3, and Hoxb-4 were expressed in very restricted domains in the future hindbrain, while Hoxb-5, Hoxb-7, and

Hoxb-9 **transcripts** were present along the entire presumptive spinal cord. It was thus notable that the 5' Hoxb genes exhibited different types of expression domain than the 3' Hoxb genes. These observations suggest that there may be different mechanisms regulating the expression of the 3' and 5' Hoxb genes. Expression of all of the Hoxb genes analyzed, except Hoxb-4, was predominantly detectable in the central nervous system or in neural crest-derived structures. Hoxb-4 **mRNA** was detected in the central nervous system, but interestingly, the major expression site for this gene was the somites. The other Hoxb genes tested failed to show significant expression in the somitic mesoderm, although **transcripts** from genes 5' from Hoxb-4 were detected in other mesodermal tissues. In the vertebrate trunk, anteroposterior patterning of the CNS is thought to be regulated by the somites. The results obtained here for Xenopus embryos did not explicitly support the idea of a Hoxb code for the somites, although we **cannot** rule this out. Instead, interestingly, the data were consistent with a role for Hoxb genes in dorsoventral patterning of the mesoderm.

L11 ANSWER 44 OF 51 MEDLINE DUPLICATE 34
ACCESSION NUMBER: 94000346 MEDLINE
DOCUMENT NUMBER: 94000346 PubMed ID: 7691069
TITLE: Retinoic acid receptor and retinoid X receptor expression in retinoic acid-resistant human tumor cell lines.
AUTHOR: van der Leede B M; van den Brink C E; van der Saag P T
CORPORATE SOURCE: Hubrecht Laboratory, Netherlands Institute for Developmental Biology, Utrecht, The Netherlands.
SOURCE: MOLECULAR CARCINOGENESIS, (1993) 8 (2) 112-22.
Journal code: 8811105. ISSN: 0899-1987.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19970203
Entered Medline: 19931119

AB Retinoic acid (RA) has profound effects on cell proliferation and differentiation both in vitro and in vivo. Many human cell lines are known to be sensitive to the growth-inhibitory action of RA. We analyzed established human solid tumor-derived cell lines for their RA sensitivity.
Growth inhibition by RA in monolayer was examined by [3H]thymidine incorporation and cell proliferation. Here we report that 11 widely used human cell lines were RA resistant. The majority are carcinoma derived (A-431, BT-20, C-41, ACHN, HCT116, 293, A549, and PA-1); two are sarcoma derived (Saos-2 and A673); and one is a melanoma cell line (A-375). Since nuclear retinoid receptors are implicated in the biological effects of RA, we examined the expression of retinoic acid receptors (RARs) RAR alpha, RAR beta, RAR gamma, and the retinoid X receptors (RXRs) RXR alpha, RXR beta, and RXR gamma in the RA-resistant cell lines by northern blotting and by RNase protection analysis for RAR beta. RAR alpha **transcripts** were constitutively expressed in all cell lines. By contrast, RAR beta was expressed in only seven RA-resistant cell lines (Saos-2, ACHN, 293, A549, A-375, A673, and PA-1), and its level was enhanced by RA in some cases. In most cell lines, RAR gamma expression was

low and was not affected by RA. The RXR genes showed a very distinct **expression pattern** in the group of selected cell lines. In general, RXR alpha was the most abundantly expressed subtype, RXR beta was expressed at low levels, and RXR gamma could not be detected. In none of the RA-resistant cell lines was RXR expression modulated by RA. The results presented here indicate that the resistance of these human tumor cell lines to RA **cannot** be simply correlated with expression of RAR or RXR or both.

L11 ANSWER 45 OF 51 MEDLINE DUPLICATE 35
ACCESSION NUMBER: 91322516 MEDLINE
DOCUMENT NUMBER: 91322516 PubMed ID: 1863773
TITLE: Patterns of gene expression in developing anthers of Brassica napus.
AUTHOR: Scott R; Dagless E; Hodge R; Paul W; Soufleri I; Draper J
CORPORATE SOURCE: Department of Botany, University of Leicester, UK.
SOURCE: PLANT MOLECULAR BIOLOGY, (1991 Aug) 17 (2) 195-207. Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199109
ENTRY DATE: Entered STN: 19910929
Last Updated on STN: 19910929
Entered Medline: 19910912

AB The relationship between bud length, anther length and stage of anther development has been investigated in Brassica napus using a series of cytological markers that define steps in the process of male gametogenesis. It was determined that bud length is directly related to anther length and that anther or bud length is tightly linked to the stage of male gametogenesis within the anther. This simple correlation has enabled the construction of **cDNA** libraries representing **transcripts** expressed in defined stages of anther development, and the detailed examination of the developmental pattern of expression of anther RNAs. Two anther **cDNA** libraries were constructed, one from anthers of 1.2-1.8 mm long buds (sporogenesis library) and one from anthers of 1.8-4.0 mm long buds (microspore development library). A total of 19 independent **cDNAs** have been isolated by differential screening whose temporal **expression patterns** overlap and which together cover the stages of anther development from pre-meiotic microsporocytes to tri-nucleate pollen grains. The pattern of expression of each of these clones is unique and indicates that stages of anther development which **cannot** be easily distinguished by light microscopy can be recognised by virtue of the absence or presence of certain RNAs. Three **cDNAs** isolated from the sporogenesis library have been shown by in situ hybridisation to be tapetum-specific. In contrast, five clones isolated from the microspore development library are microspore-specific. These clones exhibit a pattern of expression different to those previously described in that their **transcripts** are absent in mature pollen grains. Thus these RNAs are probably required in microspore development rather than for the growth of the germinating pollen grain.

L11 ANSWER 46 OF 51 MEDLINE DUPLICATE 36
ACCESSION NUMBER: 91199958 MEDLINE
DOCUMENT NUMBER: 91199958 PubMed ID: 1849812
TITLE: Retinoic acid receptors and cellular retinoid binding

proteins. II. Their differential pattern of transcription during early morphogenesis in mouse embryos.
AUTHOR: Ruberte E; Dolle P; Chambon P; Morriss-Kay G
CORPORATE SOURCE: Laboratoire de Genetique Moleculaire des Eucaryotes du CNRS. Unite 184 de Biologie Moleculaire et de Genie Genetique de l'INSERM, Strasbourg, France.
SOURCE: DEVELOPMENT, (1991 Jan) 111 (1) 45-60.
Journal code: 8701744. ISSN: 0950-1991.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199105
ENTRY DATE: Entered STN: 19910607
Last Updated on STN: 19910607
Entered Medline: 19910517

AB In situ hybridization with 35S-labelled RNA probes was used to study the distribution of **transcripts** of genes coding for the retinoic acid receptors, RAR-alpha, -beta and -gamma, and the cellular binding proteins for retinoic acid (CRABP I) and retinol (CRBP I), in mouse embryos during the period of early morphogenesis. Primary mesenchyme formation was associated with CRBP I labelling of both epiblast and mesenchyme of the primitive streak, while the CRABP probe labelled the migrating primary mesenchyme cells. Neural crest cell emigration and migration were associated with CRABP labelling of both neural epithelium (excluding the floor plate) and neural crest cells, while CRBP I expression was restricted to basal and apical regions of the epithelium (excluding the floor plate). The strongest neuroepithelial signal for CRABP was in the preoptic hindbrain. RAR-beta was present in presomitic stage embryos, being expressed at highest levels in the lateral regions. RAR-alpha was associated with crest cell emigration and migration, while RAR-gamma was present in the primitive streak region throughout the period of neurulation. There was a change from RAR-beta to RAR-gamma expression at the junction between closed and open neural epithelium at the caudal neuropore. RAR-alpha and RAR-beta were expressed at specific levels of the hindbrain and in the spinal cord. These distribution patterns are discussed in relation to segmental **expression patterns** of other genes, and to maturational changes in the caudal neuropore region. The CRABP **transcript** distribution patterns correlated well with known target tissues of excess retinoid-induced teratogenesis (migrating primary mesenchyme and neural crest cells, preoptic hindbrain), providing further support for our hypothesis that cells expressing CRABP are those that **cannot** tolerate high levels of RA for their normal developmental function.

L11 ANSWER 47 OF 51 MEDLINE DUPLICATE 37
ACCESSION NUMBER: 90099348 MEDLINE
DOCUMENT NUMBER: 90099348 PubMed ID: 2532363
TITLE: Isolation of cDNA clones encoding small nuclear ribonucleoparticle-associated proteins with different tissue specificities.
AUTHOR: Li S; Klein E S; Russo A F; Simmons D M; Rosenfeld M G
CORPORATE SOURCE: Eukaryotic Regulatory Biology Program, School of Medicine, University of California, San Diego, La Jolla 92093.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1989 Dec) 86 (24) 9778-82.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M29293; GENBANK-M29294; GENBANK-M29295
ENTRY MONTH: 199002
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19900328
Entered Medline: 19900201

AB Alternative RNA processing, such as brain- and heart-specific generation of calcitonin gene-related peptide (CGRP) **transcripts** from the calcitonin/CGRP gene, is thought to be mediated by tissue-specific factors. We have cloned three related but distinct **cDNAs** encoding small nuclear ribonucleoparticle (snRNP)-associated proteins from rat PC12 cells. One clone (Sm51) has the capacity to encode a 240-amino acid protein and its RNA **transcript** is expressed selectively in rat brain and pituitary but not in heart. A related **cDNA**, designated Sm11, predicts a protein highly homologous to but distinct from Sm51. The Sm11 **transcript** is very abundant in heart but barely detectable in brain. Sm51 and Sm11 appear to encode the brain and heart forms of a 28-kDa snRNP-associated protein detected by anti-Sm serum, respectively. A third clone (Sm21) encodes a protein with an altered N terminus relative to Sm51. The Sm51 **transcript** is expressed in the pituitary, and analysis of the pituitaries of transgenic mice harboring a mouse metallothionein I promoter-calcitonin/CGRP fusion gene reveals the splice choice to be predominantly CGRP. In situ hybridization indicates Sm51 RNA is expressed throughout neuronal structures within rat brain, including the inferior colliculus, which does not possess the machinery to generate CGRP. Although Sm51 alone **cannot** be sufficient to account for CGRP splicing choice in all tissues, the demonstration of discrete tissue-specific **expression patterns** of closely related snRNP-associated proteins is consistent with their potential role in differential RNA processing events.

L11 ANSWER 48 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:334981 BIOSIS
DOCUMENT NUMBER: BA88:37981
TITLE: HEAT SHOCK PROTEIN HSP70 COGNATE GENE EXPRESSION IN VEGETATIVE AND REPRODUCTIVE ORGANS OF LYCOPERSICON-ESCULENTUM.
AUTHOR(S): DUCK N; MCCORMICK S; WINTER J
CORPORATE SOURCE: DEP. BIOCHEM., UNIV. MISSOURI, COLUMBIA, MO. 65211.
SOURCE: PROC NATL ACAD SCI U S A, (1989) 86 (10), 3674-3678.
CODEN: PNASA6. ISSN: 0027-8424.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB We have detected hsc70 gene expression (heat shock protein hsp70 cognate) during vegetative growth and reproductive development in tomato (Lycopersicon esculentum). Using RNA from a tomato hsc70 **cDNA** as a probe in in situ hybridizations, we have determined **expression patterns** of hsc70 in nonstressed tomato roots, stems, leaves, flowers, and developing fruits. We have localized high levels of hsc70 **transcript** to the vascular system of the ovary, dividing cells of the lateral root tips, and the inner integument of developing seeds. We also see expression in the transmitting tissue, in immature anthers, and in embryos. We **cannot** detect expression in mature pollen, xylem, or ovules. These data indicate that the expression of at least some tomato hsp70 family members is developmentally regulated.

L11 ANSWER 49 OF 51 MEDLINE DUPLICATE 38
ACCESSION NUMBER: 90038548 MEDLINE
DOCUMENT NUMBER: 90038548 PubMed ID: 2478634
TITLE: Molecular basis of Qa-11 antigen and paradoxical Qa-gene expression in an H-2 recombinant.
AUTHOR: Soloski M J; Oudshoorn-Snoek M; Einhorn G; Demant P
CORPORATE SOURCE: Division of Molecular and Clinical Rheumatology, Johns Hopkins School of Medicine, Baltimore, MD 21205.
CONTRACT NUMBER: AI20922 (NIAID)
RR05378 (NCRR)
SOURCE: JOURNAL OF IMMUNOLOGY, (1989 Nov 1) 143 (9) 3074-80.
Journal code: 2985117R. ISSN: 0022-1767.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 198911
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19970203
Entered Medline: 19891130

AB The Qa-11 Ag expressed in certain strains with the B2-microglobulin-b allele, apparently maps into the Tla region as well as into the Qa-2 region. Moreover Qa-11 has been shown to be biochemically indistinguishable from Qa-2. Genetic complementation studies combining the right Qa and Tla regions failed to lead to Qa-11 expression. To elucidate the molecular basis of this apparent paradox, we examined the expression of Qa-11 on products of transfected Q-region class I genes. Immunochemical analysis has shown that the Qa-11 Ag is expressed on class I molecules encoded by the Q7 gene from both C57BL/10 (Q7b) and BALB/c (Q7d), but not on the protein product of the Q9 gene isolated from the C57BL/10 strain (Q9b). Inasmuch as the predicted protein products of the Q7b and Q9b genes would differ at a single amino acid, a residue critical for Qa-11 expression has been identified. Based on these results it is proposed that among the beta-2-mb strains, the Qa-11+/Qa-2+ mice are likely to express at least the Q7 gene, whereas Qa-11-/Qa-2+ mice express only Q9. In support of this model, the Qa-2+/Q-11- recombinant B6.K2, essential for the apparent mapping of Qa-11 into the Tla region, expresses only Q9 but not Q7 encoded molecules on the cell surface, and only Q9 and no processed Q7 **mRNA** is detected in the cytoplasm. This **expression pattern** in B6.K2 **cannot** be explained on the basis of a single crossing-over event.

L11 ANSWER 50 OF 51 MEDLINE
ACCESSION NUMBER: 90380394 MEDLINE
DOCUMENT NUMBER: 90380394 PubMed ID: 2484341
TITLE: Use of a new strategy to isolate and characterize 436 Drosophila cDNA clones corresponding to RNAs detected in adult heads but not in early embryos.
AUTHOR: Palazzolo M J; Hyde D R; VijayRaghavan K; Mecklenburg K; Benzer S; Meyerowitz E
CORPORATE SOURCE: Division of Biology, California Institute of Technology, Pasadena 91125.
CONTRACT NUMBER: GM20927 (NIGMS)
GM40499 (NIGMS)
SOURCE: NEURON, (1989 Oct) 3 (4) 527-39.

Journal code: 8809320. ISSN: 0896-6273.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199010
ENTRY DATE: Entered STN: 19901122
Last Updated on STN: 19970203
Entered Medline: 19901019

AB We describe a new strategy for producing tissue-specific **cDNA** libraries and subsequently identifying tissue-specific clones. This method was used to screen for **cDNA** clones corresponding to RNAs expressed in the Drosophila head that **cannot** be detected in the early embryo. RNA blots were used to assess the spatial and temporal patterns of expression of these RNAs. The ensemble of 436 head-not-embryo clones identified roughly 700 distinct RNAs that are differentially expressed in the Drosophila head. The RNA **expression patterns** can be classified into five major categories. it is argued that this ensemble of clones represents a large fraction of all genes differentially expressed in the adult head, but not detected in the early embryo. Many of these genes are likely to encode eye- and nervous system-specific products.

L11 ANSWER 51 OF 51 MEDLINE DUPLICATE 39
ACCESSION NUMBER: 87102629 MEDLINE
DOCUMENT NUMBER: 87102629 PubMed ID: 2433029
TITLE: Expression of the protooncogenes c-myc, c-fos, and c-fms in acute myelocytic leukemia at diagnosis and in remission.
AUTHOR: Preisler H D; Kinniburgh A J; Wei-Dong G; Khan S
CONTRACT NUMBER: CA-41285 AM-31675 (NCI)
SOURCE: CANCER RESEARCH, (1987 Feb 1) 47 (3) 874-80.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198703
ENTRY DATE: Entered STN: 19900302
Last Updated on STN: 19970203
Entered Medline: 19870304

AB RNA **transcript** levels of the protooncogenes c-myc, c-fos, and c-fms were measured in bone marrow cells obtained from patients with acute myelocytic leukemia at diagnosis or in complete remission. As controls, normal bone marrow cells were studied. The c-myc RNA levels are significantly higher in acute myelocytic leukemia cells at diagnosis than in remission or in normal marrow cells. In most instances the high c-myc RNA levels are a reflection of the high proportion of immature cells present in leukemic marrows. The bone marrow cells of several patients contain extremely high levels of c-myc RNA, levels which **cannot** be accounted for by the proportion of immature cells present in the bone marrow. The leukemic cells of patients with morphologically indistinguishable leukemias manifest different patterns of c-myc, c-fos, and c-fms expression. This observation is consistent with differences in behavior of leukemic cells even among patients with the same French-American-British type of leukemia. The normal-appearing bone marrow cells of some acute myelocytic leukemia patients in complete remission differ from normal bone marrow cells in having slightly higher c-myc RNA

levels, as well as in the pattern of expression of c-fos and c-fms. The possible use of protooncogene **expression patterns** to subdivide the French-American-British categories of acute myelocytic leukemia into subtypes with greater prognostic significance is discussed.

```
=> log h
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                      83.66      83.87

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 12:16:38 ON 09 JUL 2002


Welcome to STN International!  Enter x:x

LOGINID:ssspta1600kxc

PASSWORD:
 * * * * * * RECONNECTED TO STN INTERNATIONAL * * * * * *
SESSION RESUMED IN FILE 'MEDLINE, BIOSIS' AT 12:23:34 ON 09 JUL 2002
FILE 'MEDLINE' ENTERED AT 12:23:34 ON 09 JUL 2002
FILE 'BIOSIS' ENTERED AT 12:23:34 ON 09 JUL 2002
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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                      83.66      83.87

=> s (expression(a)pattern#)
L12      28138 (EXPRESSION(A) PATTERN#)

=> s l12(5a)(predict? or anticipat?)
L13        110 L12(5A)(PREDICT? OR ANTICIPAT?)

=> s l13 and database#
L14         12 L13 AND DATABASE#

=> dup rem l14
PROCESSING COMPLETED FOR L14
L15           7 DUP REM L14 (5 DUPLICATES REMOVED)

=> d ibib abs tot

L15  ANSWER 1 OF 7     MEDLINE                          DUPLICATE 1
ACCESSION NUMBER:   2001239781     MEDLINE
DOCUMENT NUMBER:    21233103   PubMed ID: 11335932
TITLE:              Characterization of a novel gene expressed in
neuromuscular
                    tissues and centrosomes in Caenorhabditis elegans.
AUTHOR:             Kwon S; Song W K; Park C S; Ahnn J
CORPORATE SOURCE:   Department of Life Science, Kwangju Institute of Science
                    and Technology, Kwangju, 500-712, Korea.
SOURCE:             CELL BIOCHEMISTRY AND FUNCTION, (2001 Jun) 19 (2) 79-88.
                    Journal code: 8305874. ISSN: 0263-6484.
PUB. COUNTRY:       England: United Kingdom
                    Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200109
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ENTRY DATE: Entered STN: 20010917
Last Updated on STN: 20010917
Entered Medline: 20010913

AB The nematode Caenorhabditis elegans has many advantages for studying gene function at the organism level. In particular, completion of the genome sequencing has made it feasible to study gene structure and function of both known and novel proteins. As a result of a **database** search for muscle-specific genes, a gene F43D9.1 was found which showed muscle-specific expression as revealed by the in situ hybridization pattern from the Expressed Sequence Tag (EST) **database**. A homology search of F43D9.1 protein sequences showed no significant homology with other known proteins, except that it showed very weak sequence similarity with the band 4.1 protein superfamily. Northern blot analysis reveals a single transcript 3.7 kb in size which is consistent with the **predicted** gene structure. The **expression pattern** of F43D9.1 was investigated using the gfp reporter gene, and it has shown to be expressed in neuronal cells including sensory neurons and interneurons in the head region. To further characterize F43D9.1, whole-mount immunostaining was performed with anti-F43D9.1 antibody, which showed specific signals in head neurons, body-wall muscle cells, some other unidentified neuronal cells, and centrosomes of the dividing cells during embryogenesis. Taken together with its predicted membrane topology, we speculate that the F43D9.1 gene, which encodes a novel transmembrane protein and contains a band 4.1-like domain, may function in neuromuscular cells, and may play an important role during cell division in C. elegans.

L15 ANSWER 2 OF 7 MEDLINE
ACCESSION NUMBER: 2000456114 MEDLINE
DOCUMENT NUMBER: 20296924 PubMed ID: 10835597
TITLE: Who's your neighbor? New computational approaches for functional genomics.
AUTHOR: Galperin M Y; Koonin E V
CORPORATE SOURCE: National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda MD 20894, USA.
SOURCE: NATURE BIOTECHNOLOGY, (2000 Jun) 18 (6) 609-13.
Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20001005
Last Updated on STN: 20001005
Entered Medline: 20000925

AB Several recently developed computational approaches in comparative genomics go beyond sequence comparison. By analyzing phylogenetic profiles of protein families, domain fusions, gene adjacency in genomes, and **expression patterns**, these methods **predict** many functional interactions between proteins and help deduce specific functions for numerous proteins. Although some of the resultant predictions may not be highly specific, these developments herald a new era in genomics in which the benefits of comparative analysis of the rapidly growing collection of complete genomes will become increasingly obvious.

L15 ANSWER 3 OF 7 MEDLINE
ACCESSION NUMBER: 2001085369 MEDLINE

DOCUMENT NUMBER: 20441420 PubMed ID: 10987136
TITLE: Analysis of expressed sequence tags from Brassica rapa L. ssp. pekinensis.
AUTHOR: Lim J Y; Shin C S; Chung E J; Kim J S; Kim H U; Oh S J; Choi W B; Ryou C S; Kim J B; Kwon M S; Chung T Y; Song S I; Kim J K; Nahm B H; Hwang Y S; Eun M Y; Lee J S; Cheong J J; Choi Y D
CORPORATE SOURCE: School of Agricultural Biotechnology, Seoul National University, Suwon, Korea.
SOURCE: MOLECULES AND CELLS, (2000 Aug 31) 10 (4) 399-404. Journal code: 9610936. ISSN: 1016-8478.
PUB. COUNTRY: KOREA (SOUTH)
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010118

AB Non-redundant expressed sequence tags (ESTs) were generated from six different organs at various developmental stages of Chinese cabbage, Brassica rapa L. ssp. pekinensis. Of the 1,295 ESTs, 915 (71%) showed significantly high homology in nucleotide or deduced amino acid sequences with other sequences deposited in **databases**, while 380 did not show similarity to any sequences. Briefly, 598 ESTs matched with proteins of identified biological function, 177 with hypothetical proteins or non-annotated Arabidopsis genome sequences, and 140 with other ESTs. About 82% of the top-scored matching sequences were from Arabidopsis or Brassica, but overall 558 (43%) ESTs matched with Arabidopsis ESTs at the nucleotide sequence level. This observation strongly supports the idea that gene-expression profiles of Chinese cabbage differ from that of Arabidopsis, despite their genome structures being similar to each other. Moreover, sequence analyses of 21 Brassica ESTs revealed that their primary structure is different from those of corresponding annotated sequences of Arabidopsis genes. Our data suggest that direct **prediction** of Brassica gene **expression pattern** based on the information from Arabidopsis genome research has some limitations. Thus, information obtained from the Brassica EST study is useful not only for understanding of unique developmental processes of the plant, but also for the study of Arabidopsis genome structure.

L15 ANSWER 4 OF 7 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1999419259 MEDLINE
DOCUMENT NUMBER: 99419259 PubMed ID: 10487876
TITLE: Prediction of eukaryotic mRNA translational properties.
AUTHOR: Kochetov A V; Ponomarenko M P; Frolov A S; Kisselev L L; Kolchanov N A
CORPORATE SOURCE: Institute of Cytology and Genetics, Pr. Lavrentieva 10, Novosibirsk, 630090 and Engelhardt Institute of Molecular Biology, Moscow, 117984, Russia.. AK@bionet.nsc.ru
SOURCE: BIOINFORMATICS, (1999 Jul-Aug) 15 (7-8) 704-12. Journal code: 9808944. ISSN: 1367-4803.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199912

ENTRY DATE: Entered STN: 20000114
Last Updated on STN: 20000114
Entered Medline: 19991230

AB MOTIVATION: It is well known that eukaryotic mRNAs are translated at different levels depending on their sequence characteristics. Evaluation of mRNA translatability is of importance in **prediction** of the gene **expression pattern** by computer methods and to improve the recognition of mRNAs within cloned nucleotide sequences. It may also be used in biotechnological experiments to optimize the expression of foreign genes in transgenic organisms. RESULTS: The sets of 5' untranslated region characteristics, significantly different between mRNAs encoding abundant and scarce polypeptides, were determined for mammals, dicot plants and monocot plants, and collected in the LEADER_RNA **database**. Computer tools for the prediction of mRNA translatability are presented. AVAILABILITY: Programs for mRNA translatability prediction are available at http://wwwmgs.bionet.nsc.ru/programs/acts2/mo_mRNA.htm (for monocots), http://wwwmgs.bionet.nsc.ru/programs/acts2/di_mRNA.htm (for dicots) and http://wwwmgs.bionet.nsc.ru/programs/acts2/ma_mRNA.htm (for mammals). The LEADER_RNA **database** may be accessed at: http://wwwmgs.bionet.nsc.ru/systems/LeaderRNA/.

L15 ANSWER 5 OF 7 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1999051185 MEDLINE
DOCUMENT NUMBER: 99051185 PubMed ID: 9831640
TITLE: Gene expression screening in Xenopus identifies molecular pathways, predicts gene function and provides a global view of embryonic patterning.
AUTHOR: Gawantka V; Pollet N; Delius H; Vingron M; Pfister R; Nitsch R; Blumenstock C; Niehrs C
CORPORATE SOURCE: Division of Molecular Embryology, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, D-69120, Heidelberg, Germany.
SOURCE: MECHANISMS OF DEVELOPMENT, (1998 Oct) 77 (2) 95-141. Journal code: 9101218. ISSN: 0925-4773.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AI031066; GENBANK-AI031067; GENBANK-AI031068; GENBANK-AI031069; GENBANK-AI031070; GENBANK-AI031071; GENBANK-AI031072; GENBANK-AI031073; GENBANK-AI031074; GENBANK-AI031075; GENBANK-AI031076; GENBANK-AI031077; GENBANK-AI031078; GENBANK-AI031079; GENBANK-AI031080; GENBANK-AI031081; GENBANK-AI031082; GENBANK-AI031083; GENBANK-AI031084; GENBANK-AI031085; GENBANK-AI031086; GENBANK-AI031087; GENBANK-AI031088; GENBANK-AI031089; GENBANK-AI031090; GENBANK-AI031091; GENBANK-AI031092; GENBANK-AI031093; GENBANK-AI031094; GENBANK-AI031095
ENTRY MONTH: 199901
ENTRY DATE: Entered STN: 19990209
Last Updated on STN: 20000303
Entered Medline: 19990122

AB In a large-scale gene expression screen 1765 randomly picked cDNAs were analyzed by whole-mount in situ hybridization in Xenopus embryos. Two hundred and seventy three unique, differentially expressed genes were identified, 204 of which are novel in Xenopus. Partial DNA sequences and expression patterns were documented and assembled into a **database**, 'AXelDB'. Approximately 30% of cDNAs analyzed represent differentially expressed genes and about 5% show highly regionalized expression. Novel

marker genes and potential developmental regulators were found. Differential expression of mitochondrial genes was observed. Marker genes were used to study regionalization of the entire gastrula as well as the tail forming region and the epidermis of the tailbud embryo. Four 'synexpression' groups representing genes with shared, complex **expression pattern** that **predict** molecular pathways involved in patterning and differentiation were identified. According to their probable functional significance these groups are designated as Delta1, Bmp4, ER-import and Chromatin group. Within synexpression groups, a likely function of genes without sequence similarity can be predicted. The results indicate that synexpression groups have strong prognostic value. A cluster analysis was made by comparing gene expression patterns to derive a novel parameter, 'tissue relatedness'. In conclusion, this study describes a semi-functional approach to investigate genes expressed during early development and provides global insight into embryonic patterning.

L15 ANSWER 6 OF 7 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 96042580 MEDLINE
DOCUMENT NUMBER: 96042580 PubMed ID: 7581456
TITLE: **Expression patterns** of **predicted** genes from the C. elegans genome sequence visualized by FISH in whole organisms.
AUTHOR: Birchall P S; Fishpool R M; Albertson D G
CORPORATE SOURCE: MRC Molecular Genetics Unit, Cambridge, England.
SOURCE: NATURE GENETICS, (1995 Nov) 11 (3) 314-20.
Journal code: 9216904. ISSN: 1061-4036.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951208
AB More than 10 megabases of contiguous genome sequence have been submitted to the **databases** by the Caenorhabditis elegans Genome Sequencing Consortium. To characterize the genes predicted from the sequence, we have developed high resolution FISH for visualization of mRNA distributions in whole animals. The high resolution and sensitivity afforded by the use of directly fluorescently labelled probes and confocal imaging permitted mRNA distributions to be recorded at the cellular and subcellular level. Expression patterns were obtained for 8 out of 10 genes in an initial test set of predicted gene sequences, indicating that FISH is an effective means of characterizing predicted genes in C. elegans.

L15 ANSWER 7 OF 7 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 96042579 MEDLINE
DOCUMENT NUMBER: 96042579 PubMed ID: 7581455
TITLE: Developmental **expression pattern** screen for genes **predicted** in the C. elegans genome sequencing project.
AUTHOR: Lynch A S; Briggs D; Hope I A
CORPORATE SOURCE: Department of Pure and Applied Biology, University of Leeds, UK.
SOURCE: NATURE GENETICS, (1995 Nov) 11 (3) 309-13.
Journal code: 9216904. ISSN: 1061-4036.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951208

AB Maximum use should be made of information generated in the genome sequencing projects. Toward this end, we have initiated a genome sequence-based, **expression pattern** screen of genes **predicted** from the Caenorhabditis elegans genome sequence data. We examined beta-galactosidase expression patterns in C. elegans lines transformed with lacZ reporter gene fusions constructed using predicted C.
elegans gene promoter regions. Of the predicted genes in the cosmids analysed so far, 67% are amenable to the approach and 54% of examined genes yielded a developmental expression pattern. Expression pattern information is being made generally available using computer **databases**.

=> d history

(FILE 'HOME' ENTERED AT 11:50:48 ON 09 JUL 2002)

FILE 'MEDLINE, BIOSIS' ENTERED AT 11:51:25 ON 09 JUL 2002
L1 14581 S EST# OR (SEQUENCE(W)TAG#)
L2 83 S L1(S)("NOT" OR CANNOT)
L3 55 DUP REM L2 (28 DUPLICATES REMOVED)
L4 13496 S EST OR ESTS OR (SEQUENCE(W)TAG#)
L5 83 S L2 (S)("NOT" OR CANNOT)
L6 82 S L4 (S)("NOT" OR CANNOT)
L7 1637565 S MRNA OR CDNA OR POLYNUCLEOTIDE# OR DNA OR TRANSCRIPT#
L8 544939 S MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#
L9 11399 S L8(S)(EXPRESSION(W)PATTERN#)
L10 90 S L9(S)(CANNOT OR "NOT")
L11 51 DUP REM L10 (39 DUPLICATES REMOVED)
L12 28138 S (EXPRESSION(A)PATTERN#)
L13 110 S L12(5A)(PREDICT? OR ANTICIPAT?)
L14 12 S L13 AND DATABASE#
L15 7 DUP REM L14 (5 DUPLICATES REMOVED)

=> s l12(3a)predict? or anticipat?)
UNMATCHED RIGHT PARENTHESIS 'ANTICIPAT?)'
The number of right parentheses in a query must be equal to the number of left parentheses.

=> s l12(3a)(predict? or anticipat?)
L16 87 L12(3A)(PREDICT? OR ANTICIPAT?)

=> dup rem l16
PROCESSING COMPLETED FOR L16
L17 50 DUP REM L16 (37 DUPLICATES REMOVED)

=> d ibib abs tot

L17 ANSWER 1 OF 50 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002054065 MEDLINE
DOCUMENT NUMBER: 21638446 PubMed ID: 11696550
TITLE: Alx4 binding to LEF-1 regulates N-CAM promoter activity.

AUTHOR: Boras Kata; Hamel Paul A
CORPORATE SOURCE: Department of Laboratory Medicine and Pathobiology, University of Toronto, Ontario M5S 1A8, Canada.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 Jan 11) 277 (2) 1120-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020208
Entered Medline: 20020207

AB During murine embryogenesis, expression of the paired-like homeodomain protein Alx4 is restricted to tissues whose development depends on the expression of lymphoid enhancer factor-1 (LEF-1). Given the defects seen in hair follicle development in both LEF-1 and Alx4 knockout and mutant animals and the overlapping **expression patterns**, we **predicted** that LEF-1 and Alx4 might form physical complexes. We demonstrate here the interaction between LEF-1 and Alx4. This interaction is mediated through a specific proline-rich domain in the N-terminal region of Alx4 and requires the DNA-binding domain (HMG-box) of LEF-1. We also demonstrate that LEF-1 and Alx4 can bind simultaneously to adjacent sites on the neural cell adhesion molecule (N-CAM) promoter and that this binding alters N-CAM promoter activity. Furthermore, when expressed in primary mammary stromal cells, Alx4 decreases the expression of endogenous N-CAM protein. These results reveal a potential mechanism that gives rise to mesenchymal-specific activities of LEF-1.

L17 ANSWER 2 OF 50 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002193052 MEDLINE
DOCUMENT NUMBER: 21903839 PubMed ID: 11906919
TITLE: Mosaic gene expression in nuclear transfer-derived embryos and the production of cloned transgenic pigs from ear-derived fibroblasts.
AUTHOR: Park Kwang-Wook; Lai Liangxue; Cheong Hee-Tae; Cabot Ryan; Sun Qing-Yuan; Wu Guangming; Rucker Edmund B; Durtschi David; Bonk Aaron; Samuel Melissa; Rieke A; Day Bill N; Murphy Clifton N; Carter D B; Prather Randall S
CORPORATE SOURCE: Department of Animal Sciences, University of Missouri-Columbia, 920 East Campus Drive, Columbia, MO 65211, USA.
CONTRACT NUMBER: R01 RR 13428 (NCRR)
T32 RR 07004 (NCRR)
SOURCE: BIOLOGY OF REPRODUCTION, (2002 Apr) 66 (4) 1001-5.
Journal code: 0207224. ISSN: 0006-3363.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020404
Last Updated on STN: 20020702
Entered Medline: 20020701

AB Genetically modified domestic animals have many potential applications ranging from basic research to production agriculture. One of the goals in transgenic animal production schemes is to reliably **predict** the **expression pattern** of the foreign gene. Establishing a

method to screen genetically modified embryos for transgene expression before transfer to surrogates may improve the likelihood of producing offspring with the desired expression pattern. In order to determine how transgene expression may be regulated in the early embryo, we generated porcine embryos from two distinct genetically modified cell lines by using the nuclear transfer (NT) technique. Both cell lines expressed the enhanced green fluorescent protein (eGFP); the first was a fibroblast cell line derived from the skin of a newborn pig that expressed eGFP, whereas the second was a fetal derived fibroblast cell line into which the eGFP gene was introduced by a retroviral vector. The reconstructed embryos were activated by electrical pulses and cultured in NCSU23. Although the in vitro developmental ability of each group of NT embryos was not different, the eGFP expression pattern was different. All embryos produced from the transduced fetal cell line fluoresced, but only 26% of the embryos generated from the newborn cell line fluoresced, and among those that did express eGFP, more than half had a mosaic expression pattern. This was unexpected because the fetal cell line was not clonally selected, and each cell had potentially different sites of integration. Embryos generated from the newborn cell line were surgically transferred to five surrogate gilts. One gilt delivered four female piglets, all of which expressed eGFP, and all had microsatellites identical to the donor. Here we demonstrate that transgene expression in all the blastomeres of an NT embryo is not uniform. In addition, transgene expression in a genetically manipulated embryo may not be an accurate indicator of expression in the resulting offspring.

L17 ANSWER 3 OF 50 MEDLINE
ACCESSION NUMBER: 2002195804 IN-PROCESS
DOCUMENT NUMBER: 21926506 PubMed ID: 11928496
TITLE: Identifying muscle regulatory elements and genes in the nematode Caenorhabditis elegans.
AUTHOR: Guhathakurta D; Schriefer L A; Hresko M C; Waterston R H; Stormo G D
CORPORATE SOURCE: Department of Genetics, Washington University School of Medicine, 4566 Scott Avenue, Campus Box 8232, St. Louis, MO 63110, USA.. dg@genetics.wustl.edu
CONTRACT NUMBER: HG00249 (NHGRI)
SOURCE: PACIFIC SYMPOSIUM ON BIOCOMPUTING, (2002) 425-36. Journal code: 9711271.
PUB. COUNTRY: Singapore
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020404
Last Updated on STN: 20020404
AB We report the identification of several putative muscle-specific regulatory elements, and genes which are expressed preferentially in the muscle of the nematode Caenorhabditis elegans. We used computational pattern finding methods to identify cis-regulatory motifs from promoter regions of a set of genes known to express preferentially in muscle; each motif describes the potential binding sites for an unknown regulatory factor. The significance and specificity of the identified motifs were evaluated using several different control sequence sets. Using the motifs, we searched the entire C. elegans genome for genes whose promoter regions

have a high probability of being bound by the putative regulatory factors.
Genes that met this criterion and were not included in our initial set were predicted to be good candidates for muscle expression. Some of these candidates are additional, known muscle expressed genes and several others
are shown here to be preferentially expressed in muscle cells by using GFP
(green fluorescent protein) constructs. The methods described here can be used to **predict** the spatial **expression pattern**
of many uncharacterized genes.

L17 ANSWER 4 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:547812 BIOSIS
DOCUMENT NUMBER: PREV200100547812
TITLE: Predicting temporal-spatial gene expression in neuronal progenitors using oligonucleotide microarrays.
AUTHOR(S): Zhao, Q. (1); Kho, A.; Kenney, A. M. (1); Yuk, D. (1); Golub, T. R.; Kohane, I.; Zhang, Y. (1); Rowitch, D. H. (1)
CORPORATE SOURCE: (1) Pediatric Oncology, Dana-Farber Cancer Institute, Boston, MA USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 1525. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The genetic mechanisms regulating proliferation and differentiation of cerebellar granule neuron precursors (CGNP) during development are poorly understood. This issue is of particular interest because CGNP are thought to be the origin of the pediatric brain tumor, medulloblastoma. We have used Affymetrix Mu11K (GeneChips) oligonucleotide microarrays to identify genes upregulated in immature granule cells in primary cultures of post-natal day 5 (PN5) cerebellum when treated with the mitogen, Sonic Hedgehog (SHH). Despite such primary cultures are highly heterogeneous and
contain only 15-20% proliferating cells, we observed a rapid upregulation (2-15 folds) of numerous genes when treated with SHH proteins. In contrast, we observed no significant increase in gene expression following
growth arrest, suggesting that the granule cells in culture are relatively
unresponsive to SHH upon cell cycle exit. Using novel analysis tools, we derived a list of genes/ESTs upregulated by Shh treatment and prospectively screened their expression pattern by in situ hybridization, RT-PCR and northern blot. This method accurately predicted gene expression
specifically in the developing external granule cell layer of the PN7 cerebellum in 78% of cases tested. These results demonstrate that appropriate in vitro models in conjunction with oligonucleotide microarrays may be used to accurately **predict** gene **expression pattern** and gene discovery in proliferating neural precursors.

L17 ANSWER 5 OF 50 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002085877 MEDLINE
DOCUMENT NUMBER: 21605281 PubMed ID: 11737781

TITLE: Distinct cell-specific expression patterns of early and late gibberellin biosynthetic genes during Arabidopsis seed germination.
AUTHOR: Yamaguchi S; Kamiya Y; Sun T
CORPORATE SOURCE: Developmental, Cell and Molecular Biology Group, Department of Biology, Duke University, Box 91000, Durham, North Carolina 27708-1000, USA.. shinjiro@postman.riken.go.jp
SOURCE: PLANT JOURNAL, (2001 Nov) 28 (4) 443-53.
Journal code: 9207397. ISSN: 0960-7412.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020130
Last Updated on STN: 20020301
Entered Medline: 20020228

AB Gibberellins (GAs) are biosynthesized through a complex pathway that involves several classes of enzymes. To predict sites of individual GA biosynthetic steps, we studied cell type-specific expression of genes encoding early and late GA biosynthetic enzymes in germinating Arabidopsis seeds. We showed that expression of two genes, AtGA3ox1 and AtGA3ox2, encoding GA 3-oxidase, which catalyzes the terminal biosynthetic step, was mainly localized in the cortex and endodermis of embryo axes in germinating seeds. Because another GA biosynthetic gene, AtKO1, coding for ent-kaurene oxidase, exhibited a similar cell-specific **expression pattern**, we **predicted** that the synthesis of bioactive GAs from ent-kaurene oxidation occurs in the same cell types during seed germination. We also showed that the cortical cells expand during germination, suggesting a spatial correlation between GA production and response. However, promoter activity of the AtCPS1 gene, responsible for the first committed step in GA biosynthesis, was detected exclusively in the embryo provasculature in germinating seeds. When the AtCPS1 cDNA was expressed only in the cortex and endodermis of non-germinating ga1-3 seeds (deficient in AtCPS1) using the AtGA3ox2 promoter, germination was not as resistant to a GA biosynthesis inhibitor as expression in the provasculature. These results suggest that the biosynthesis of GAs during seed germination takes place in two separate locations with the early step occurring in the provasculature and the later steps in the cortex and endodermis. This implies that intercellular transport of an intermediate of the GA biosynthetic pathway is required to produce bioactive GAs.

L17 ANSWER 6 OF 50 MEDLINE
ACCESSION NUMBER: 2002080060 IN-PROCESS
DOCUMENT NUMBER: 21664924 PubMed ID: 11806634
TITLE: Conservation and variation in Ubx expression among chelicerates.
AUTHOR: Popadic A; Nagy L
CORPORATE SOURCE: Department of Biological Sciences, Wayne State University, Detroit, MI 48202, USA.. apopadic@biology.biosci.wayne.edu
SOURCE: Evol Dev, (2001 Nov-Dec) 3 (6) 391-6.
Journal code: 100883432. ISSN: 1520-541X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020128
Last Updated on STN: 20020128

AB Chelicerates are an ancient arthropod group with a distinct body plan composed of an anterior (prosoma) and a posterior portion (opisthosoma). The expression of the Hox gene Ultrabithorax (Ubx) has been examined in a single representative of the chelicerates, the spider Cupiennius salei. In spiders, Ubx expression starts in the second opisthosomal segment (O2). Because the first opisthosomal segment (O1) in spiders is greatly reduced relative to other chelicerates, we hypothesized that the observed Ubx expression pattern might be secondarily modified. Shifts in the anterior boundary of the expression of Ubx have been correlated with functional shifts in morphology within malacostracan crustaceans. Thus, the boundary of Ubx expression between chelicerates with different morphologies in their anterior opisthosoma could also be variable. To test this **prediction**, we examined the **expression patterns** of Ubx and abdominal-A (collectively referred to as UbdA) in two basal chelicerate lineages, scorpions and xiphosurans (horseshoe crabs), which exhibit variation in the morphology of their anterior opisthosoma. In the scorpion Paruroctonus mesaensis, the anterior border of early expression of UbdA is in a few cells in the medial, posterior region of the O2 segment, with a predominant expression in O3 and posterior. Expression later spreads to encompass the whole O2 segment and a ventral, posterior portion of the O1 segment. In the xiphosuran Limulus polyphemus, early expression of UbdA has an anterior boundary in the segment. Later in development, the anterior boundary moves forward one segment to the chilarial (O1) segment. Thus, the earliest expression boundary of UbdA lies within the second opisthosomal segment in all the chelicerates examined. These results suggest that rather than being derived, the spider UbdA expression in O2 likely reflects the ancestral expression boundary. Changes in the morphology of the first opisthosomal segment are either not associated with changes in UbdA expression or correlate with late developmental changes in UbdA expression.

L17 ANSWER 7 OF 50 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2001126542 MEDLINE
DOCUMENT NUMBER: 21080233 PubMed ID: 11211615
TITLE: Diagnostic usefulness of CD23 and FMC-7 antigen expression patterns in B-cell lymphoma classification.
AUTHOR: Garcia D P; Rooney M T; Ahmad E; Davis B H
CORPORATE SOURCE: Departments of Clinical, William Beaumont Hospital, Royal Oak, MI, USA.
SOURCE: AMERICAN JOURNAL OF CLINICAL PATHOLOGY, (2001 Feb) 115 (2) 258-65.
Journal code: 0370470. ISSN: 0002-9173.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010222

AB CD23 and FMC-7 are normal B-cell antigens used during diagnostic immunophenotyping of suspected lymphoproliferative disorders, but the diagnostic usefulness of antigenic expression patterns of simultaneous 2-color staining and flow cytometric analysis has not been reported. We

evaluated the FMC-7 and CD23 expression pattern in 201 cases of B-cell lymphoma from tissue biopsy specimens by multiparameter flow cytometry. The CD23-/FMC-7+ pattern was the most common pattern in large cell, mantle cell, and marginal zone lymphomas. The CD23 and FMC-7 antigen, along with the CD5 coexpression pattern, permitted accurate classification of all 71 cases of small lymphocytic, mantle cell, and marginal zone types of lymphoma. The widest variation of patterns was with follicular cell lymphoma, although most cases expressed the CD23 +/-/FMC-7+ pattern (+/-, partial or minor subset expression). The CD23 and FMC-7 antigen **expression pattern** was **predictive** of subtypes in more than 95% of lymphoma cases and could narrow the differential diagnosis in the remaining cases. We conclude the flow cytometric CD23/FMC-7 expression pattern achieved by dual staining facilitates accurate and reproducible classification of B-cell lymphomas and has diagnostic usefulness.

L17 ANSWER 8 OF 50 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2001158398 MEDLINE
DOCUMENT NUMBER: 21098774 PubMed ID: 11180959
TITLE: Two sox9 genes on duplicated zebrafish chromosomes: expression of similar transcription activators in distinct sites.
AUTHOR: Chiang E F; Pai C I; Wyatt M; Yan Y L; Postlethwait J; Chung B
CORPORATE SOURCE: Institute of Molecular Biology, Academia Sinica, Nankang, Taiwan, Republic of China.
CONTRACT NUMBER: R01RR10715 (NCRR)
SOURCE: DEVELOPMENTAL BIOLOGY, (2001 Mar 1) 231 (1) 149-63. Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010322

AB Sox9 is a transcription factor required for cartilage formation and testis determination in mammals. We have cloned from zebrafish two sox9 genes, termed sox9a and sox9b. Gene phylogenies showed that both genes are orthologous to tetrapod SOX9 genes. Genetic mapping showed that these two loci reside on chromosome segments that were apparently duplicated in a large-scale genomic duplication event in ray fin fish phylogeny. Both Sox9a and Sox9b proteins bind to the HMG consensus DNA sequences in vitro. We tested different domains for transactivation potential and identified a potential activation domain located in the middle of both Sox9a and Sox9b. During embryogenesis, sox9a and sox9b expression patterns are distinct but overlap in some regions of the brain, head skeleton, and fins. Expression of sox9a/b correlates well with that of col2a1 in chondrogenic elements. In the adults, sox9a is expressed in many tissues including brain, muscle, fin, and testis, whereas sox9b expression is restricted to previtellogenic oocytes of the ovary. This **expression pattern** **predicts** that sox9a and sox9b may have unique functions in some

specific tissues during development. The role of gene duplication for the evolution of developmental gene function is discussed.

L17 ANSWER 9 OF 50 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2001239781 MEDLINE
DOCUMENT NUMBER: 21233103 PubMed ID: 11335932
TITLE: Characterization of a novel gene expressed in neuromuscular tissues and centrosomes in Caenorhabditis elegans.
AUTHOR: Kwon S; Song W K; Park C S; Ahnn J
CORPORATE SOURCE: Department of Life Science, Kwangju Institute of Science and Technology, Kwangju, 500-712, Korea.
SOURCE: CELL BIOCHEMISTRY AND FUNCTION, (2001 Jun) 19 (2) 79-88. Journal code: 8305874. ISSN: 0263-6484.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200109
ENTRY DATE: Entered STN: 20010917
Last Updated on STN: 20010917
Entered Medline: 20010913

AB The nematode Caenorhabditis elegans has many advantages for studying gene function at the organism level. In particular, completion of the genome sequencing has made it feasible to study gene structure and function of both known and novel proteins. As a result of a database search for muscle-specific genes, a gene F43D9.1 was found which showed muscle-specific expression as revealed by the in situ hybridization pattern from the Expressed Sequence Tag (EST) database. A homology search of F43D9.1 protein sequences showed no significant homology with other known proteins, except that it showed very weak sequence similarity with the band 4.1 protein superfamily. Northern blot analysis reveals a single transcript 3.7 kb in size which is consistent with the **predicted** gene structure. The **expression pattern** of F43D9.1 was investigated using the gfp reporter gene, and it has shown to be expressed in neuronal cells including sensory neurons and interneurons in the head region. To further characterize F43D9.1, whole-mount immunostaining was performed with anti-F43D9.1 antibody, which showed specific signals in head neurons, body-wall muscle cells, some other unidentified neuronal cells, and centrosomes of the dividing cells during embryogenesis. Taken together with its predicted membrane topology, we speculate that the F43D9.1 gene, which encodes a novel transmembrane protein and contains a band 4.1-like domain, may function in neuromuscular cells, and may play an important role during cell division in C. elegans.

L17 ANSWER 10 OF 50 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001243162 MEDLINE
DOCUMENT NUMBER: 21100873 PubMed ID: 11161794
TITLE: Identification and characterization of a SET/NAP protein encoded by a brain-specific gene, MB20.
AUTHOR: Shen H H; Huang A M; Hoheisel J; Tsai S F
CORPORATE SOURCE: Institute of Genetics, National Yang Ming University, Taipei, 112, Republic of China.
SOURCE: GENOMICS, (2001 Jan 1) 71 (1) 21-33. Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB010711
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010510

AB A new member of the NAP/SET gene family, named MB20, was isolated from a mouse brain cDNA library by virtue of its CAG trinucleotide repetitive sequence and a brain-specific gene expression pattern. The complementary DNA sequence predicted an open reading frame of 545 amino acids, with four copies of an 11-amino-acid direct repeat. The consensus sequence for these repeats, PKE-P--K-EE, is present in the largest subunit of murine neurofilament (NF-H). The MB20 protein sequence is homologous to nucleosome assembly proteins of several species, and its C-terminus is homologous to SET proteins. Immunoblot analysis revealed that MB20 protein is expressed in the brain. Transient transfection and immunofluorescence microscopy demonstrated that MB20 is distributed in the cytoplasm as well as in the nucleus. Deletion of the N-terminal end imparts the complete localization of MB20 protein to the nucleus. The ability of MB20 to bind histone proteins was analyzed by sucrose gradient sedimentation and by retention of histone proteins by immobilized MB20 protein. On the basis of its **expression pattern**, **predicted** sequence, and protein properties, we propose that MB20 plays a unique role in modulating nucleosome structure and gene expression during brain development.

L17 ANSWER 11 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:106838 BIOSIS
DOCUMENT NUMBER: PREV200100106838
TITLE: Gene expression patterns in pediatric sarcomas as a predictor of clinical outcome.
AUTHOR(S): Schofield, D. (1); Mjolsness, E.; Buckley, J.; Wold, B.; Triche, T. J.
CORPORATE SOURCE: (1) University of Southern California Keck School of Medicine, Los Angeles, CA USA
SOURCE: Laboratory Investigation, (January, 2001) Vol. 81, No. 1, pp. 18A. print.
Meeting Info.: Annual Meeting of the United States and Canadian Academy of Pathology Atlanta, Georgia, USA March 03-09, 2001
ISSN: 0023-6837.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L17 ANSWER 12 OF 50 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2000396594 MEDLINE
DOCUMENT NUMBER: 20347155 PubMed ID: 10749877
TITLE: Expression analysis of BACE2 in brain and peripheral tissues.
AUTHOR: Bennett B D; Babu-Khan S; Loeloff R; Louis J C; Curran E; Citron M; Vassar R
CORPORATE SOURCE: Amgen, Inc., Thousand Oaks, California 91320-1799, USA.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Jul 7) 275 (27) 20647-51.
Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF204944
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000816

AB Beta-site amyloid precursor protein cleaving enzyme (BACE) is a novel transmembrane aspartic protease that possesses all the known characteristics of the beta-secretase involved in Alzheimer's disease (Vassar, R., Bennett, B. D., Babu-Khan, S., Kahn, S., Mendiaz, E. A., Denis, P., Teplow, D. B., Ross, S., Amarante, P., Loeloff, R., Luo, Y., Fisher, S., Fuller, J., Edenson, S., Lile, J., Jarosinski, M. A., Biere, A. L., Curran, E., Burgess, T., Louis, J. -C., Collins, F., Treanor, J., Rogers, G., and Citron, M. (1999) Science 286, 735-741). We have analyzed the sequence and expression pattern of a BACE homolog termed BACE2. BACE and BACE2 are unique among aspartic proteases in that they possess a carboxyl-terminal extension with a predicted transmembrane region and together they define a new family. Northern analysis reveals that BACE2 mRNA is expressed at low levels in most human peripheral tissues and at higher levels in colon, kidney, pancreas, placenta, prostate, stomach, and trachea. Human adult and fetal whole brain and most adult brain subregions express very low or undetectable levels of BACE2 mRNA. In addition, in situ hybridization of adult rat brain shows that BACE2 mRNA is expressed at very low levels in most brain regions. The very low or undetectable levels of BACE2 mRNA in the brain are not consistent with the **expression pattern predicted** for beta-secretase.

L17 ANSWER 13 OF 50 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2000300943 MEDLINE
DOCUMENT NUMBER: 20300943 PubMed ID: 10823904
TITLE: Decoupled evolution of coding region and mRNA expression patterns after gene duplication: implications for the neutralist-selectionist debate.
AUTHOR: Wagner A
CORPORATE SOURCE: The Santa Fe Institute, University of New Mexico, Department of Biology, 167A Castetter Hall, Albuquerque, NM 87131-1091, USA.. wagnera@unm.edu
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2000 Jun 6) 97 (12) 6579-84. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000713

AB The neutralist perspective on molecular evolution maintains that the vast majority of mutations affecting gene function are neutral or deleterious. After a gene duplication where both genes are retained, it predicts that original and duplicate genes diverge at clock-like rates. This prediction is usually tested for coding sequences, but can also be applied to another

important aspect of gene function, the genes' expression pattern. Moreover, if both sequence and expression pattern diverge at clock-like rates, a correlation between divergence in sequence and divergence in expression patterns is expected. Duplicate gene pairs with more highly diverged sequences should also show more highly diverged **expression patterns**. This **prediction** is tested for a large sample of duplicated genes in the yeast Saccharomyces cerevisiae, using both genome sequence and microarray expression data. Only a weak correlation is observed, suggesting that coding sequence and mRNA expression patterns of duplicate gene pairs evolve independently and at vastly different rates. Implications of this finding for the neutralist-selectionist debate are discussed.

L17 ANSWER 14 OF 50 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2000456114 MEDLINE
DOCUMENT NUMBER: 20296924 PubMed ID: 10835597
TITLE: Who's your neighbor? New computational approaches for functional genomics.
AUTHOR: Galperin M Y; Koonin E V
CORPORATE SOURCE: National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda MD 20894, USA.
SOURCE: NATURE BIOTECHNOLOGY, (2000 Jun) 18 (6) 609-13. Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20001005
Last Updated on STN: 20001005
Entered Medline: 20000925
AB Several recently developed computational approaches in comparative genomics go beyond sequence comparison. By analyzing phylogenetic profiles of protein families, domain fusions, gene adjacency in genomes, and **expression patterns**, these methods **predict** many functional interactions between proteins and help deduce specific functions for numerous proteins. Although some of the resultant predictions may not be highly specific, these developments herald a new era in genomics in which the benefits of comparative analysis of the rapidly growing collection of complete genomes will become increasingly obvious.

L17 ANSWER 15 OF 50 MEDLINE
ACCESSION NUMBER: 2001085369 MEDLINE
DOCUMENT NUMBER: 20441420 PubMed ID: 10987136
TITLE: Analysis of expressed sequence tags from Brassica rapa L. ssp. pekinensis.
AUTHOR: Lim J Y; Shin C S; Chung E J; Kim J S; Kim H U; Oh S J; Choi W B; Ryou C S; Kim J B; Kwon M S; Chung T Y; Song S I; Kim J K; Nahm B H; Hwang Y S; Eun M Y; Lee J S; Cheong J J; Choi Y D
CORPORATE SOURCE: School of Agricultural Biotechnology, Seoul National University, Suwon, Korea.
SOURCE: MOLECULES AND CELLS, (2000 Aug 31) 10 (4) 399-404. Journal code: 9610936. ISSN: 1016-8478.
PUB. COUNTRY: KOREA (SOUTH)
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010118

AB Non-redundant expressed sequence tags (ESTs) were generated from six different organs at various developmental stages of Chinese cabbage, Brassica rapa L. ssp. pekinensis. Of the 1,295 ESTs, 915 (71%) showed significantly high homology in nucleotide or deduced amino acid sequences with other sequences deposited in databases, while 380 did not show similarity to any sequences. Briefly, 598 ESTs matched with proteins of identified biological function, 177 with hypothetical proteins or non-annotated Arabidopsis genome sequences, and 140 with other ESTs. About 82% of the top-scored matching sequences were from Arabidopsis or Brassica, but overall 558 (43%) ESTs matched with Arabidopsis ESTs at the nucleotide sequence level. This observation strongly supports the idea that gene-expression profiles of Chinese cabbage differ from that of Arabidopsis, despite their genome structures being similar to each other. Moreover, sequence analyses of 21 Brassica ESTs revealed that their primary structure is different from those of corresponding annotated sequences of Arabidopsis genes. Our data suggest that direct **prediction** of Brassica gene **expression pattern** based on the information from Arabidopsis genome research has some limitations. Thus, information obtained from the Brassica EST study is useful not only for understanding of unique developmental processes of the plant, but also for the study of Arabidopsis genome structure.

L17 ANSWER 16 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:70934 BIOSIS
DOCUMENT NUMBER: PREV200100070934
TITLE: Can gene **expression pattern** analysis **predict** recurrence in node-negative breast cancer.
AUTHOR(S): Immaneni, A.; Li, Z.; Hilsenbeck, S. G.; Allred, D. C.; O'Connell, P.
SOURCE: Breast Cancer Research and Treatment, (November, 2000) Vol. 64, No. 1, pp. 101. print.
Meeting Info.: 23rd Annual San Antonia Breast Cancer Symposium San antonio, Texas, USA December 06-09, 2000
ISSN: 0167-6806.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L17 ANSWER 17 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:97907 BIOSIS
DOCUMENT NUMBER: PREV200100097907
TITLE: LAR PTP receptor: coordination of expression patterns within neural networks.
AUTHOR(S): Longo, F. M. (1); Yeo, T. T.
CORPORATE SOURCE: (1) VAMC V-127, San Francisco, CA USA
SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-509.7. print.
Meeting Info.: 30th Annual Meeting of the Society of Neuroscience New Orleans, LA, USA November 04-09, 2000 Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference

LANGUAGE: English
SUMMARY LANGUAGE: English
AB Insect and transgenic mice studies suggest that protein tyrosine phosphatases (PTPs) regulate establishment of neural networks. We have found aberrant hippocampal innervation in mice deficient in the leukocyte common antigen-related (LAR) PTP receptor, and that the extracellular domain of LAR undergoes homophilic interaction and promotes neurite outgrowth. These findings generated the hypothesis that LAR contributes to the formation and/or maintenance of neural networks and **predicted** that **expression patterns** would reflect such networks. Using adult transgenic mice expressing a LAR-driven beta-galactosidase/neomycin (beta-geo) reporter gene, a detailed survey of LAR/beta-geo fusion protein expression was performed. LAR/beta-geo expression was abundant in limbic and paralimbic systems that provide input to and serve as targets for the hippocampus. Hippocampal afferents included: entorhinal cortex, amygdala, septum, hypothalamic, mammillary and raphe nuclei. Hippocampal targets included: olfactory regions, amygdala, septum, hypothalamic and mammillary nuclei. High levels of LAR/beta-geo were present in CA3 with increasing staining along the anterior-posterior axis suggesting a topographic distribution. The majority of afferents and targets of the olfactory bulb also had abundant staining. LAR/beta-geo expression was present in vestibular nucleus-associated input and target regions including: Purkinje cells, deep cerebellar nuclei, spinal dorsal horn layers and DRG neurons. Within the cortex, specific layers expressing LAR/beta-geo varied in a markedly distinct topographical manner. These findings support the hypothesis that LAR plays an important role in formation, maintenance and/or function of neural networks.

L17 ANSWER 18 OF 50 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 2000016313 MEDLINE
DOCUMENT NUMBER: 20016313 PubMed ID: 10547558
TITLE: Antiapoptotic Bcl-2 family protein expression increases with progression of oligodendroglioma.
AUTHOR: Deininger M H; Weller M; Streffer J; Meyermann R
CORPORATE SOURCE: Institute of Brain Research, University of Tubingen Medical School, Tubingen, Germany.
SOURCE: CANCER, (1999 Nov 1) 86 (9) 1832-9.
Journal code: 0374236. ISSN: 0008-543X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991223
AB BACKGROUND: Altered expression of Bcl-2 family proteins has been associated with tumorigenesis and tumor progression as well as resistance to radiotherapy and chemotherapy. In the current study, Bcl-2 family protein expression was examined in oligodendrogliomas and anaplastic oligodendrogliomas, and an attempt was made to determine whether these proteins accumulate during disease progression and to search for protein **expression patterns predictive** of time to progression and overall survival. METHODS: A total of 42 oligodendroglioma tissue samples, 26 de novo World Health Organization (WHO) Grade 2 oligodendrogliomas, and 16 de novo WHO Grade 3 anaplastic oligodendrogliomas were studied. Nineteen Grade 2 tumors progressed: 10

again were Grade 2 oligodendrogliomas and 8 had progressed to higher grade lesions. Eight anaplastic oligodendrogliomas progressed: five again were WHO Grade 3 tumors and three were glioblastoma multiforme. Expression of Bcl-2, Bax, Bcl-X, and Mcl-1 proteins and of the proliferation marker Ki-67 was evaluated by immunohistochemistry. Apoptotic cells were quantified by in situ nick translation (ISNT). RESULTS: De novo WHO Grade 2 oligodendrogliomas had higher Bcl-2 scores (P = 0.037), lower MIB-1 scores (P = 0.0012), and lower ISNT scores (P = 0.049) compared with de novo WHO Grade 3 anaplastic oligodendrogliomas. In de novo oligodendrogliomas, low numbers of Bax positive cells were associated with a short time to disease progression (P = 0.043). In de novo anaplastic oligodendrogliomas, low numbers of Bcl-2 positive cells correlated with short survival (P = 0.029). In tumors that had progressed from WHO Grade 3 anaplastic oligodendrogliomas, the authors found significantly more Bcl-X positive (P = 0.005), Mcl-1 positive (P = 0.002), and Bax positive (P = 0.03) cells. CONCLUSIONS: The results of the current study show that progression of oligodendrogliomas and anaplastic oligodendrogliomas is associated with an enhanced expression of antiapoptotic Bcl-2 family proteins.

L17 ANSWER 19 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2000:151151 BIOSIS
DOCUMENT NUMBER: PREV200000151151
TITLE: Otic placode fate map suggests cell mixing is more predominant than **predicted** by gene **expression patterns**.
AUTHOR(S): Kil, S. H. (1); Collazo, A. (1)
CORPORATE SOURCE: (1) Dept. of Cell and Molecular Biology, House Ear Institute, Los Angeles, CA, 90057 USA
SOURCE: Society for Neuroscience Abstracts., (1999) Vol. 25, No. 1-2, pp. 753.
Meeting Info.: 29th Annual Meeting of the Society for Neuroscience. Miami Beach, Florida, USA October 23-28, 1999
Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L17 ANSWER 20 OF 50 MEDLINE DUPLICATE 12

ACCESSION NUMBER: 1999419259 MEDLINE
DOCUMENT NUMBER: 99419259 PubMed ID: 10487876
TITLE: Prediction of eukaryotic mRNA translational properties.
AUTHOR: Kochetov A V; Ponomarenko M P; Frolov A S; Kisselev L L; Kolchanov N A
CORPORATE SOURCE: Institute of Cytology and Genetics, Pr. Lavrentieva 10, Novosibirsk, 630090 and Engelhardt Institute of Molecular Biology, Moscow, 117984, Russia.. AK@bionet.nsc.ru
SOURCE: BIOINFORMATICS, (1999 Jul-Aug) 15 (7-8) 704-12.
Journal code: 9808944. ISSN: 1367-4803.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000114

Last Updated on STN: 20000114
Entered Medline: 19991230

AB MOTIVATION: It is well known that eukaryotic mRNAs are translated at different levels depending on their sequence characteristics. Evaluation of mRNA translatability is of importance in **prediction** of the gene **expression pattern** by computer methods and to improve the recognition of mRNAs within cloned nucleotide sequences. It may also be used in biotechnological experiments to optimize the expression of foreign genes in transgenic organisms. RESULTS: The sets of 5' untranslated region characteristics, significantly different between mRNAs encoding abundant and scarce polypeptides, were determined for mammals, dicot plants and monocot plants, and collected in the LEADER_RNA database. Computer tools for the prediction of mRNA translatability are presented. AVAILABILITY: Programs for mRNA translatability prediction are available at http://wwwmgs.bionet.nsc. ru/programs/acts2/mo_mRNA.htm (for monocots), http://wwwmgs.bionet. nsc.ru/programs/acts2/di_mRNA.htm (for dicots) and http://wwwmgs. bionet.nsc.ru/programs/acts2/ma_mRNA.htm (for mammals). The LEADER_RNA database may be accessed at: http://wwwmgs.bionet.nsc. ru/systems/LeaderRNA/.

L17 ANSWER 21 OF 50 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 1999229296 MEDLINE
DOCUMENT NUMBER: 99229296 PubMed ID: 10212826
TITLE: Cytokeratin expression patterns in normal and malignant urothelium: a review of the biological and diagnostic implications.
AUTHOR: Southgate J; Harnden P; Trejdosiewicz L K
CORPORATE SOURCE: ICRF Cancer Medicine Research Unit, Research School of Medicine, St James's University Hospital, Leeds, UK.. j.southgate@leeds.ac.uk
SOURCE: HISTOLOGY AND HISTOPATHOLOGY, (1999 Apr) 14 (2) 657-64. Ref: 56
Journal code: 8609357. ISSN: 0213-3911.
PUB. COUNTRY: Spain
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990714
Last Updated on STN: 19990714
Entered Medline: 19990628

AB The cytokeratins are the intermediate filament proteins characteristic of epithelial cells. In human cells, some 20 different cytokeratin isotypes have been identified. Epithelial cells express between two and ten cytokeratin isotypes and the consequent profile which reflects both epithelial type and differentiation status may be useful in tumour diagnosis. The transitional epithelium or urothelium of the urinary tract shows alterations in the expression and configuration of cytokeratin isotypes related to stratification and differentiation. In transitional cell carcinoma, changes in cytokeratin profile may provide information of potential diagnostic and prognostic significance. The intensification of immunolabelling with some CK8 and CK18 antibodies may underly an active role in tumour invasion and foci of CK17-positive cells may represent proliferating populations. Loss of CK13 is a marker of grade and stage and
de novo expression of CK14 is indicative of squamous differentiation and an unfavourable prognosis. However, perhaps the most important recent finding is the demonstration that a normal CK20 **expression pattern** is **predictive** of tumour non-recurrence and can

be used to make an objective differential diagnosis between transitional cell papilloma and carcinoma. This review will consider cytokeratin expression in urothelium and discuss the application of cytokeratin typing to the diagnosis and prognosis of patients with TCC.

L17 ANSWER 22 OF 50 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 2000093425 MEDLINE
DOCUMENT NUMBER: 20093425 PubMed ID: 10632569
TITLE: Expression of VEGF splice variants 144/145 and 205/206 in adult male tissues.
AUTHOR: Burchardt T; Burchardt M; Chen M W; Buttyan R; de la Taille A; Shabsigh A; Shabsigh R
CORPORATE SOURCE: Department of Urology, College of Physicians and Surgeons of Columbia University, New York, New York 10032, USA.
SOURCE: IUBMB Life, (1999 Oct) 48 (4) 405-8.
Journal code: 100888706. ISSN: 1521-6543.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000218
Last Updated on STN: 20000218
Entered Medline: 20000209

AB Currently, at least five different mRNA species encoding vascular endothelial growth factor-A (VEGF-A) have been characterized. These variants result from alternative splicing of the VEGF-A transcript and encode human isoforms of VEGF protein of 121, 145, 165, 189, and 206 amino acids. In the rat, a similar profile of VEGF-A splice variants has been described, each encoding one fewer amino acid than the human species. Studies of mammalian tissues have shown that these mRNA isoforms vary in abundance. Whereas VEGF 188/189, 164/165, and 120/121 (rat/human, respectively) are the predominant forms expressed in most tissues and cells examined, VEGF 144/145 and 205/206 are rare variants. Previously, VEGF 144/145 had been detected only in placental and uterine tissues and endometrial carcinoma cell lines, whereas VEGF 205/206 was detected only in fetal liver and placenta. Using an RT-PCR technique, cDNA cloning, and sequencing, we have detected and confirmed the presence of mRNA encoding VEGF 144/145 and 205/206 in both adult rat lung and penis. Therefore, these low-abundance VEGF splice variants have a more diverse **expression pattern** than originally **predicted**.

L17 ANSWER 23 OF 50 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 1999065492 MEDLINE
DOCUMENT NUMBER: 99065492 PubMed ID: 9847235
TITLE: A new family of growth factors produced by the fat body and active on Drosophila imaginal disc cells.
AUTHOR: Kawamura K; Shibata T; Saget O; Peel D; Bryant P J
CORPORATE SOURCE: Developmental Biology Center, University of California, Irvine, Irvine, CA 92717, USA.. kazuk@cc.kochi-u.ac.jp
SOURCE: DEVELOPMENT, (1999 Jan) 126 (2) 211-9.
Journal code: 8701744. ISSN: 0950-1991.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF102236; GENBANK-AF102237; GENBANK-AF102238;

GENBANK-AF102239
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 19990324
Entered Medline: 19990308

AB By fractionating conditioned medium (CM) from Drosophila imaginal disc cell cultures, we have identified a family of Imaginal Disc Growth Factors (IDGFs), which are the first polypeptide growth factors to be reported from invertebrates. The active fraction from CM, as well as recombinant IDGFs, cooperate with insulin to stimulate the proliferation, polarization and motility of imaginal disc cells. The IDGF family in Drosophila includes at least five members, three of which are encoded by three genes in a tight cluster. The proteins are structurally related to chitinases, but they show an amino acid substitution that is known to abrogate catalytic activity. It therefore seems likely that they have evolved from chitinases but acquired a new growth-promoting function. The IDGF genes are expressed most strongly in the embryonic yolk cells and in the fat body of the embryo and larva. The **predicted** molecular structure, **expression patterns**, and mitogenic activity of these proteins suggest that they are secreted and transported to target tissues via the hemolymph. However, the genes are also expressed in embryonic epithelia in association with invagination movements, so the proteins may have local as well as systemic functions. Similar proteins are found in mammals and may constitute a novel class of growth factors.

L17 ANSWER 24 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:61603 BIOSIS
DOCUMENT NUMBER: PREV200000061603
TITLE: MUC genes: A superfamily of genes? Varied structures and **expression patterns predict** diverse and specific functions.
AUTHOR(S): Porchet, Nicole (1); Buisine, Marie-Pierre; Desseyn, Jean-Luc; Moniaux, Nicolas; Nollet, Severine; Degand, Pierre; Pigny, Pascal; Van Seuningen, Isabelle; Laine, Anne; Aubert, Jean-Pierre
CORPORATE SOURCE: (1) Unite INSERM, n 377, Place de Verdun, 59045, Lille Cedex France
SOURCE: Journal de la Societe de Biologie, (1999) Vol. 193, No. 1, pp. 85-99.
ISSN: 1295-0661.
DOCUMENT TYPE: General Review
LANGUAGE: French
SUMMARY LANGUAGE: English; French

AB The MUC genes encode epithelial mucins. Eight different human genes have been well characterized, and two others identified more recently. Among them, a family of four genes, expressed in the respiratory and digestive tracts, is clustered to chromosome 11p15.5; and these genes encode gel-forming mucins which are structurally related to the superfamily of cystine-knot growth factors. A second group is composed of three independent genes encoding various isoforms of mucins including membrane-bound mucins associated to carcinomas. In this second group, MUC3 and MUC4 encode large apomucins containing EGF-like domains.

L17 ANSWER 25 OF 50 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 1999137394 MEDLINE
DOCUMENT NUMBER: 99137394 PubMed ID: 9973109
TITLE: Suppression of the tumorigenicity of prostatic cancer cells

by gene(s) located on human chromosome 19p13.1-13.2.

AUTHOR: Gao A C; Lou W; Ichikawa T; Denmeade S R; Barrett J C; Isaacs J T

CORPORATE SOURCE: Johns Hopkins Oncology Center, Department of Urology, Johns Hopkins University School of Medicine, Baltimore, Maryland 21231, USA.

CONTRACT NUMBER: CA 58236 (NCI)

SOURCE: PROSTATE, (1999 Jan 1) 38 (1) 46-54.
Journal code: 8101368. ISSN: 0270-4137.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199902

ENTRY DATE: Entered STN: 19990311
Last Updated on STN: 19990311
Entered Medline: 19990223

AB BACKGROUND: In previous reports, we used microcell fusion-mediated chromosomal transfer to introduce normal human chromosomes into highly metastatic rat prostatic cancer cells to map the location of tumor and metastasis suppressor genes. The gene for prostate-specific antigen as well as several classes of genes, including cell adhesion molecules, previously demonstrated to be altered during prostate cancer progression, were mapped to human chromosome 19. METHODS: A normal human chromosome 19 was introduced into Dunning-R3327 AT6.1 rat and TSU-prl human prostatic cancer cells by microcell-mediated chromosome transfer to test the suppressive effects of this chromosome on prostate cancer. Five independent hybrid clones from Dunning-R3327 AT6.1 rat prostatic cancer cells and four independent hybrid clones from TSU-pr1 human prostatic cancer cells were isolated, karyotyped, allelotyped, and analyzed for in vitro and in vivo growth characteristics. RESULTS: Introduction of human chromosome 19 into both the rat and human prostatic cancer cells resulted in alteration of cell morphology in vitro and suppression of tumorigenicity in vivo in athymic nude mice. Highly polymorphic SSR2 markers mapped to human chromosome 19 were used to determine the portions of human chromosome 19 retained in the hybrids. These analyses identified a region localized on human chromosome 19p13.1-13.2 that is responsible for the tumor suppression of both rat and human prostatic cancer cells. The expression of several genes previously mapped to this human chromosome 19p13.1-13.2 region (i.e., ICAM-1, Notch3, and Stau) were analyzed to evaluate if they could be candidate suppressor genes for prostate cancer cell growth in vivo, but no **expression patterns** consistent with those **predicted** for a suppressor gene were observed. CONCLUSIONS: Human chromosome 19p13.1-13.2 contains potential tumor suppressor gene(s) for prostate cancer.

L17 ANSWER 26 OF 50 MEDLINE DUPLICATE 17

ACCESSION NUMBER: 1999141329 MEDLINE

DOCUMENT NUMBER: 99141329 PubMed ID: 9973545

TITLE: Expression patterns of folate binding proteins one and two in the developing mouse embryo.

AUTHOR: Barber R C; Bennett G D; Greer K A; Finnell R H

CORPORATE SOURCE: Department of Veterinary Anatomy and Public Health, Texas A&M University, College Station, Texas, 77843-4458, USA.

CONTRACT NUMBER: ES07165 (NIEHS)
HD/ES35396 (NICHD)
P30-E509106

SOURCE: MOLECULAR GENETICS AND METABOLISM, (1999 Jan) 66 (1) 31-9.
Journal code: 9805456. ISSN: 1096-7192.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 19990324
Entered Medline: 19990311

AB Expression patterns of mRNAs coding for the murine folate binding proteins one and two (FBP1 and FBP2) were determined by ribonuclease protection assay (RPA) in highly inbred SWV/Fnn mouse embryos. Tissue samples for RPA were collected from the anterior neural tube throughout the period of embryonic development, as well as from maternal- and fetal-derived term placenta. The peak in expression of FBP1 occurred in term placental tissue compared to neural tissue from any time point. This relative increase in FBP1 expression occurred in placental tissue of embryonic, as opposed to maternal, origin. The expression of FBP2 did not differ statistically between any timepoints or tissues examined. Expression of both FBP1 and FBP2 was slightly elevated throughout the period of neural tube closure (Gestational Days 8 through 10), although not significantly. These data fit the **anticipated expression patterns** of the homologues of human folate receptors alpha and beta, thus helping to resolve some of the confusion secondary to the nomenclature associated with this gene family. Furthermore, the expression of these two genes in the neural tube closure stage of embryological development supports their involvement in regulatory events related to normal neural tube morphogenesis.

L17 ANSWER 27 OF 50 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 1999077301 MEDLINE
DOCUMENT NUMBER: 99077301 PubMed ID: 9862485
TITLE: Promoter trapping identifies real genes in C. elegans.
AUTHOR: Hope I A; Arnold J M; McCarroll D; Jun G; Krupa A P; Herbert R
CORPORATE SOURCE: School of Biology, The University of Leeds, UK.. i.a.hope@leeds.ac.uk
SOURCE: MOLECULAR AND GENERAL GENETICS, (1998 Nov) 260 (2-3) 300-8.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199901
ENTRY DATE: Entered STN: 19990128
Last Updated on STN: 19990128
Entered Medline: 19990114

AB Promoter trapping involved screening uncharacterized fragments of C. elegans genomic DNA for C. elegans promoter activity. By sequencing the ends of these DNA fragments and locating their genomic origin using the available genome sequence data, promoter trapping has now been shown to identify real promoters of real genes, exactly as **anticipated**. Developmental **expression patterns** have thereby been linked to gene sequence, allowing further inferences on gene function to be drawn. Some expression patterns generated by promoter trapping include subcellular details. Localization to the surface of particular cells or even particular aspects of the cell surface was found to be consistent

with the genes, now associated with these patterns, encoding membrane-spanning proteins. Data on gene expression patterns are easier to generate and characterize than mutant phenotypes and may provide the best means of interpreting the large quantity of sequence data currently being generated in genome projects.

L17 ANSWER 28 OF 50 MEDLINE DUPLICATE 19

ACCESSION NUMBER: 1999051185 MEDLINE
DOCUMENT NUMBER: 99051185 PubMed ID: 9831640
TITLE: Gene expression screening in Xenopus identifies molecular pathways, predicts gene function and provides a global view of embryonic patterning.
AUTHOR: Gawantka V; Pollet N; Delius H; Vingron M; Pfister R; Nitsch R; Blumenstock C; Niehrs C
CORPORATE SOURCE: Division of Molecular Embryology, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, D-69120, Heidelberg, Germany.
SOURCE: MECHANISMS OF DEVELOPMENT, (1998 Oct) 77 (2) 95-141. Journal code: 9101218. ISSN: 0925-4773.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AI031066; GENBANK-AI031067; GENBANK-AI031068; GENBANK-AI031069; GENBANK-AI031070; GENBANK-AI031071; GENBANK-AI031072; GENBANK-AI031073; GENBANK-AI031074; GENBANK-AI031075; GENBANK-AI031076; GENBANK-AI031077; GENBANK-AI031078; GENBANK-AI031079; GENBANK-AI031080; GENBANK-AI031081; GENBANK-AI031082; GENBANK-AI031083; GENBANK-AI031084; GENBANK-AI031085; GENBANK-AI031086; GENBANK-AI031087; GENBANK-AI031088; GENBANK-AI031089; GENBANK-AI031090; GENBANK-AI031091; GENBANK-AI031092; GENBANK-AI031093; GENBANK-AI031094; GENBANK-AI031095
ENTRY MONTH: 199901
ENTRY DATE: Entered STN: 19990209
Last Updated on STN: 20000303
Entered Medline: 19990122

AB In a large-scale gene expression screen 1765 randomly picked cDNAs were analyzed by whole-mount in situ hybridization in Xenopus embryos. Two hundred and seventy three unique, differentially expressed genes were identified, 204 of which are novel in Xenopus. Partial DNA sequences and expression patterns were documented and assembled into a database, 'AXelDB'. Approximately 30% of cDNAs analyzed represent differentially expressed genes and about 5% show highly regionalized expression. Novel marker genes and potential developmental regulators were found. Differential expression of mitochondrial genes was observed. Marker genes were used to study regionalization of the entire gastrula as well as the tail forming region and the epidermis of the tailbud embryo. Four 'synexpression' groups representing genes with shared, complex **expression pattern** that **predict** molecular pathways involved in patterning and differentiation were identified. According to their probable functional significance these groups are designated as Delta1, Bmp4, ER-import and Chromatin group. Within synexpression groups, a likely function of genes without sequence similarity can be predicted. The results indicate that synexpression groups have strong prognostic value. A cluster analysis was made by comparing gene expression patterns to derive a novel parameter, 'tissue relatedness'. In conclusion, this study describes a semi-functional approach to investigate genes expressed during early development and

provides global insight into embryonic patterning.

L17 ANSWER 29 OF 50 MEDLINE DUPLICATE 20

ACCESSION NUMBER: 1998381541 MEDLINE
DOCUMENT NUMBER: 98381541 PubMed ID: 9715752
TITLE: **Prediction** of mutant **expression patterns** using gene circuits.
AUTHOR: Sharp D H; Reinitz J
CORPORATE SOURCE: Theoretical Division, Los Alamos National Laboratory, NM 87545, USA.. dhs@t13.lanl.gov
CONTRACT NUMBER: RO1-RR07801 (NCRR)
SOURCE: BIOSYSTEMS, (1998 Jun-Jul) 47 (1-2) 79-90.
Journal code: 0430773. ISSN: 0303-2647.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981104

AB Networks of interacting transcription factors, or gene circuits, form an essential part of the metabolic pathways controlling macromolecular synthesis. This paper conveys two new results about gene circuits. We first show how a gene circuit for mutant phenotypes can be constructed from the wild type gene circuit for the same organism. We then present results of computational studies that show that mutant **expression patterns** can be correctly **predicted** using gene circuits whose parameters have been determined from wild type data only. Further computational studies demonstrate that this property is insensitive to errors as large as a factor of two in the input data. Together, these results show that gene circuits can be used to identify the regulatory mechanisms governing an entire family of genotypes from a knowledge of the wild type genotype alone. It is argued that this fact forms the basis for a new paradigm in genetics.

L17 ANSWER 30 OF 50 MEDLINE DUPLICATE 21

ACCESSION NUMBER: 1998193127 MEDLINE
DOCUMENT NUMBER: 98193127 PubMed ID: 9524219
TITLE: Isolation and characterization of a cDNA encoding a high mobility group protein HMG-1 from Canavalia gladiata D.C.
AUTHOR: Yamamoto S; Minamikawa T
CORPORATE SOURCE: Department of Biology, Tokyo Metropolitan University, Japan.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1998 Mar 4) 1396 (1) 47-50.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB000637
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980430
Last Updated on STN: 19980430
Entered Medline: 19980421

AB A cDNA clone encoding a HMG-1 protein from maturing seeds of Canavalia gladiata was isolated and characterized with respect to its sequence, genomic organization and the **expression pattern** in

seeds. The **predicted** polypeptide had the characteristic conserved motifs of the HMG-1/2 protein including N-terminal basic region, one HMG-box and polyacidic carboxy terminus. Southern blot analysis suggested that the HMG-1 gene is a single copy gene. Northern blot analysis indicated that the HMG-1 gene was expressed both in maturing and germinated seeds.

L17 ANSWER 31 OF 50 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 97268657 MEDLINE
DOCUMENT NUMBER: 97268657 PubMed ID: 9108065
TITLE: Gypsy retrotransposon as a tool for the in vivo analysis of the regulatory region of the optomotor-blind gene in Drosophila.
AUTHOR: Tsai S F; Jang C C; Prikhod'ko G G; Bessarab D A; Tang C Y; Pflugfelder G O; Sun Y H
CORPORATE SOURCE: Institute of Genetics, National Yang-Ming University, Taipei, Taiwan.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1997 Apr 15) 94 (8) 3837-41. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970602
Last Updated on STN: 20000303
Entered Medline: 19970522

AB We report here a method for the in vivo dissection of the regulatory region of a gene in the Drosophila genome. Our system includes (i) the reporter genes lacZ and white to detect transcriptional enhancer and silencer activities in a target gene, (ii) an efficient way to induce integration of gypsy elements in the genome, and (iii) unidirectional blocking of regulatory activities by the gypsy element, which is dependent on the su(Hw) protein. The optomotor-blind (omb) gene was analyzed. In the omb(P1) line, a P[lacW] construct is inserted about 1.4 kb upstream of the omb transcription start site. The lacZ reporter gene within P[lacW] exhibits the same expression pattern as omb. The white reporter gene is expressed in a "bipolar" pattern. We induced high frequency gypsy mobilization in omb(P1) and identified two lines (D11 and D13-1) with altered eye pigmentation pattern, which is dependent on su(Hw) activity. A gypsy element was found inserted in the first intron of omb in D13-1 and in P[lacW] in D11. These results indicate that it is the blocking of regulatory activities by gypsy that caused the changes in the white reporter gene expression. The effect of these gypsy insertions on the **expression patterns** allowed us to **predict** several aspects of the organization of the regulatory elements in the omb locus.

L17 ANSWER 32 OF 50 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 97424605 MEDLINE
DOCUMENT NUMBER: 97424605 PubMed ID: 9278718
TITLE: Modelling the activity of the Ultrabithorax parasegment-specific regulatory domains around their

anterior boundaries.

AUTHOR: Singh P B; Brown D
CORPORATE SOURCE: Department of Development and Genetics, Babraham Institute, Cambridge, U.K.
SOURCE: JOURNAL OF THEORETICAL BIOLOGY, (1997 Jun 21) 186 (4) 397-413.
Journal code: 0376342. ISSN: 0022-5193.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199709
ENTRY DATE: Entered STN: 19971008
Last Updated on STN: 19971008
Entered Medline: 19970919

AB The Drosophila Ultrabithorax (Ubx) gene was one of the first homeotic genes to be characterised and it specifies the phenotypic characteristics of parasegments 5 and 6. The intricate pattern of Ubx expression in these parasegments is conferred by enormous regulatory regions which, together with the structural gene, constitute the Ubx domain. A genetic, "open-for-business", model based on classical mutational analysis proposed that the regulatory regions were in fact composite structures, consisting of parasegment-specific regulatory domains that contain arrays of cell-specific enhancers which drive the intricate pattern of Ubx expression. Here, we propose a molecular mechanism, based on a survey of numerous transgenic studies, of the setting up of these parasegment-specific regulatory domains in the appropriate parts of the late blastoderm embryo. We construct a mathematical model of this mechanism using the molecular characteristics of a single initiator element, the distributions of segmentation gene products and simple competitive binding equations. We attempt to fit this mathematical model to the idealised patterns of activity and closure of the parasegment-specific domains derived from the genetic model. The resulting fitted pattern of activity and closure obtained with the simplest version of our competitive binding model shows some deviations from the idealised pattern based on the genetic model. Comparison of the predictions with recent experimental evidence suggests that the competitive binding model more accurately reflects certain features of the Ubx **expression pattern**--features not **predicted** by the genetic model.

L17 ANSWER 33 OF 50 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 97464078 MEDLINE
DOCUMENT NUMBER: 97464078 PubMed ID: 9322769
TITLE: Cloning and molecular characterization of an Arabidopsis thaliana RING zinc finger gene expressed preferentially during seed development.
AUTHOR: Zou J; Taylor D C
CORPORATE SOURCE: National Research Council of Canada, Plant Biotechnology Institute, Saskatchewan, Canada.
SOURCE: GENE, (1997 Sep 1) 196 (1-2) 291-5.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U81598
ENTRY MONTH: 199710
ENTRY DATE: Entered STN: 19971224

Last Updated on STN: 19971224
Entered Medline: 19971030

AB The RING (Really Interesting New Gene) finger is a zinc-binding domain that is found in proteins from a variety of species. This paper reports the cloning and characterization of, as yet, only the second RING finger protein gene from plants, A-RZE, in Arabidopsis thaliana. In addition to the RING-finger motif, A-RZF also contains a putative nuclear localization signal. A-RZF is encoded by a single copy gene with an intron of 595 bp interrupting the 5' leader sequence and the coding region. Northern blot analysis indicated that A-RZF is expressed preferentially during seed development. The RING-finger motif, putative nuclear localization signal, and unique **expression pattern**, **predict** an important role during seed development for A-RZF.

L17 ANSWER 34 OF 50 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 96323121 MEDLINE
DOCUMENT NUMBER: 96323121 PubMed ID: 8709227
TITLE: CD4 down-modulation during infection of human T cells with human immunodeficiency virus type 1 involves independent activities of vpu, env, and nef.
AUTHOR: Chen B K; Gandhi R T; Baltimore D
CORPORATE SOURCE: Department of Biology, Massachusetts Institute of Technology, Cambridge 02139, USA.
SOURCE: JOURNAL OF VIROLOGY, (1996 Sep) 70 (9) 6044-53.
Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; AIDS
ENTRY MONTH: 199609
ENTRY DATE: Entered STN: 19960919
Last Updated on STN: 19970203
Entered Medline: 19960910

AB The human immunodeficiency virus type 1 (HIV-1) genes vpu, env, and nef have all been implicated in modulating the levels of cell surface CD4 on infected cells. To quantitatively assess the relative contribution of each gene product to the regulation of CD4 during HIV infection of Jurkat T cells and peripheral blood mononuclear cells, we have developed an infectious HIV reporter system which expresses different combinations of these genes. To distinguish infected cells in the early or late stages of infection from uninfected cells, these viruses were designed to express human placental alkaline phosphatase with the kinetics of either early or late viral genes. Flow cytometry to detect placental alkaline phosphatase and CD4 in infected cells showed that vpu, env, and nef are independently capable of down-modulation of CD4. As **predicted** by their respective **expression patterns**, nef down-modulated CD4 rapidly during the early phase of virus infection whereas vpu and env functioned late in the infection. In both Jurkat cells and peripheral blood mononuclear cells, a combination of the three genes was more efficient than any one or two genes, demonstrating that all three genes are required to achieve maximal CD4 down-modulation. In primary cells, down-modulation of CD4 was less efficient than in Jurkat cells and there was a stronger dependence on nef function for reducing cell surface CD4. HIV therefore has three genes that are able to independently down-modulate CD4; together, they can eliminate the bulk of cell surface CD4.

L17 ANSWER 35 OF 50 MEDLINE DUPLICATE 26
ACCESSION NUMBER: 96424461 MEDLINE

DOCUMENT NUMBER: 96424461 PubMed ID: 8826984
TITLE: Cloning, tissue expression, and chromosomal localization of
SUR2, the putative drug-binding subunit of cardiac, skeletal muscle, and vascular KATP channels.
AUTHOR: Chutkow W A; Simon M C; Le Beau M M; Burant C F
CORPORATE SOURCE: Department of Medicine, Howard Hughes Medical Institute, Chicago, Illinois, USA.
CONTRACT NUMBER: CA67021 (NCI)
DK-02170 (NIDDK)
RO1 HL52094 (NHLBI)
+
SOURCE: DIABETES, (1996 Oct) 45 (10) 1439-45.
Journal code: 0372763. ISSN: 0012-1797.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
OTHER SOURCE: GENBANK-AF003531; GENBANK-U97066
ENTRY MONTH: 199611
ENTRY DATE: Entered STN: 19961219
Last Updated on STN: 20000303
Entered Medline: 19961104

AB ATP-sensitive inwardly rectifying potassium channels are expressed in a variety of tissues, including heart, skeletal, and smooth muscle, and pancreatic beta-cells. Physiological and pharmacological studies suggest the presence of distinct KATP channels in these tissues. Recently, the KATP channel of beta-cells has been reconstituted in functional form by coexpression of SUR, the sulfonylurea-binding protein, and the inwardly rectifying K+ channel subunit, KIR6.2. In this article, we describe the isolation of cDNAs encoding SUR-like proteins from mouse, SUR2A and SUR2B.

Northern blotting showed that the highest expression of the SUR2 isoforms is in the heart and skeletal muscle, with lower levels in all other tissues. By reverse transcription-polymerase chain reaction, SUR2B is ubiquitously expressed, while the apparently alternatively spliced variant, SUR2A, is expressed exclusively in heart. In situ hybridization shows that the SUR2 isoforms are expressed in the parenchyma of the heart and skeletal muscle and in the vascular structures of other tissues.

Human SUR2 was localized to chromosome 12, p12.1 by fluorescent in situ hybridization. The structure of the **predicted** protein and **expression pattern** of SUR2 suggests that it is the drug-binding channel-modulating subunit of the extrapancreatic KATP channel. Differences in sequence between SUR and between SUR2 isoforms may underlie the tissue-specific pharmacology of the KATP channel.

L17 ANSWER 36 OF 50 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 97128093 MEDLINE
DOCUMENT NUMBER: 97128093 PubMed ID: 8972754
TITLE: Can malignancy in insulinoma be **predicted** by the **expression patterns** of beta 1,6 branching of asparagine-linked oligosaccharides and polysialic acid of the neural cell adhesion molecule?.
AUTHOR: Li W P; Komminoth P; Zuber C; Kloppel G; Heitz P U; Roth J
CORPORATE SOURCE: Department of Pathology, University of Zurich, Switzerland.
SOURCE: VIRCHOWS ARCHIV, (1996 Nov) 429 (4-5) 197-204.
Journal code: 9423843. ISSN: 0945-6317.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19970114

AB We analysed the value of the expression of beta 1,6 branching of asparagine-linked oligosaccharide chains and polysialic acid of the neural cell adhesion molecule (NCAM) in predicting malignant behaviour in human insulinomas, as these glycoconjugates have been associated with invasive growth and metastatic potential. Fifty-three insulinomas from patients with well-documented clinical and follow-up data were investigated. Lectin histochemical staining for beta 1,6 branches revealed that 11 (74%) of the 15 malignant insulinomas stained more strongly than normal beta cells. However, in as many as 23 (63.1%) of the 38 benign insulinomas with a disease-free follow up for 4-18 years (average 8 years), a staining intensity equivalent to that of malignant tumours was found. Two (13%) of the malignant insulinomas and 1 of the 4 liver metastases studied were unstained. None of the 53 insulinomas (and the rat RIN insulinoma) re-expressed polysialic acid as demonstrated by immunohistochemistry and Western blotting with the monoclonal antibody 735. Therefore, histochemical staining for beta 1,6 branches and immunohistochemistry for polysialic acid are unlikely to be of value as prognostic indicators for patients with insulinomas.

L17 ANSWER 37 OF 50 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 96108891 MEDLINE
DOCUMENT NUMBER: 96108891 PubMed ID: 8613720
TITLE: Regional patterns of c-fos mRNA expression in rat hippocampus following exploration of a novel environment versus performance of a well-learned discrimination.
AUTHOR: Hess U S; Lynch G; Gall C M
CORPORATE SOURCE: Department of Psychobiology, University of California at Irvine 92717, USA.
CONTRACT NUMBER: HD24236 (NICHD)
MH00358 (NIMH)
MH00974 (NIMH)
+
SOURCE: JOURNAL OF NEUROSCIENCE, (1995 Dec) 15 (12) 7796-809.
Journal code: 8102140. ISSN: 0270-6474.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199606
ENTRY DATE: Entered STN: 19960613
Last Updated on STN: 19960613
Entered Medline: 19960606

AB Previous studies using c-fos cRNA in situ hybridization demonstrated a differential involvement of hippocampal subfields CA1 and CA3 in the acquisition of an olfactory discrimination (Hess et al., 1995). The present experiments employed the same method to examine changes in neuronal activity associated with two related behaviors: (1) initial exploration of the training apparatus and (2) performance of a well-learned odor discrimination. Rats in the two groups had similar labeling patterns within hippocampus indicating increased expression in all three major subfields with the greatest effect being in CA1. This

pattern of "CA1 dominance" was notably different from that produced during early stages of two-odor discrimination learning in prior experiments. Hippocampal labeling in exploration and performance rats differed in that (1) hybridization was greater in CA1, CA3, and dentate gyrus in the former group and (2) a tendency for labeled cells to occur in clusters was more evident in exploration animals. Levels of c-fos mRNA in olfactory and visual structures were not **predictive** of **expression patterns** within hippocampus although labeling in piriform cortex and dentate gyrus was correlated in rats performing a well-practiced discrimination. Moreover, the pattern of hybridization in olfactory bulb was found to be behaviorally dependent. These results, together with those from previous studies, indicate that hippocampus has multiple patterns of regional activation but that one of these is common to very different behavioral circumstances. It is hypothesized that this common pattern emerges whenever the animal responds to distant cues using species-specific or well-learned behaviors and involves coordinated temporal convergence of sensory and septal/brainstem inputs.

L17 ANSWER 38 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1996:112056 BIOSIS
DOCUMENT NUMBER: PREV199698684191
TITLE: Two major mechanisms regulating cell-fate decisions in the developing nervous system.
AUTHOR(S): Okano, Hideyuki
CORPORATE SOURCE: Dep. Mol. Neurobiol., Inst. Basic Med. Sci., Univ. Tsukuba, 1-1-1 Ten-noudai, Tsukuba 305 Japan
SOURCE: Development Growth & Differentiation, (1995) Vol. 37, No. 6, pp. 619-629.
ISSN: 0012-1592.
DOCUMENT TYPE: General Review
LANGUAGE: English

AB Two types of determinants appear to be responsible for the generation of neural cell diversity: non-cell-autonomous and cell-autonomous cues. We have identified both types of determinants through the intensive screening of P-element induced Drosophila mutants affected in neural development. As a member of the first category argos (also referred to as strawberry or giant lens), which regulates cell-cell interaction in the developing nervous system, needs to be mentioned. On the basis of the phenotype on loss of function of argos, its **expression pattern** and the **predicted** structure of its product (a secreted protein with a putative epidermal growth factor (EGF) motif) we propose that argos encodes a diffusible protein with pleiotropic functions that acts as a signal involved in lateral inhibition within the developing nervous system and also as a factor involved in axonal guidance. As a member of the second category, I refer to the Drosophila musashi gene that is required for lineage formation and asymmetric division of precursor cells in the developing nervous system. The musashi gene encodes a neural RNA-biding protein and is thus likely to regulate the asymmetric cell division of neural precursor cells by controlling the expression of target genes at the post-transcriptional level. We have identified its mammalian homologue, mouse-musashi-1 (m-Msi-1). In the developing central nervous system (CNS), m-Msi-1 expression was highly enriched to neural precursor cells as is the expression of nestin. Based on the results of a single cell culture experiment, m-Msi-1 expression appears to be associated with

multipotent cells that are capable of self-renewal and with the generation of committed precursor cells of both neurons and glia. However, fully differentiated neuronal and glial cells lost their m-Msi-1 expression. The expression of m-Msi protein showed a complementary pattern to that of another mammalian RNA-binding protein Hu, which is localized in differentiated neurons in the CNS. Based on such differential expression patterns and its similarity to the Drosophila musashi, we propose that a combination of neural RNA-binding proteins are required for the asymmetric distribution of intrinsic determinants in the developing mammalian nervous system. The Drosophila glial-specific homeobox protein, Repo, can also be classified as a cell-autonomous cue regulating cell-fate decision during neural development. Repo expression is required for terminal differentiation and for the survival of glial cells.

L17 ANSWER 39 OF 50 MEDLINE DUPLICATE 29
ACCESSION NUMBER: 96042580 MEDLINE
DOCUMENT NUMBER: 96042580 PubMed ID: 7581456
TITLE: **Expression patterns** of **predicted** genes from the C. elegans genome sequence visualized by FISH in whole organisms.
AUTHOR: Birchall P S; Fishpool R M; Albertson D G
CORPORATE SOURCE: MRC Molecular Genetics Unit, Cambridge, England.
SOURCE: NATURE GENETICS, (1995 Nov) 11 (3) 314-20.
Journal code: 9216904. ISSN: 1061-4036.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951208

AB More than 10 megabases of contiguous genome sequence have been submitted to the databases by the Caenorhabditis elegans Genome Sequencing Consortium. To characterize the genes predicted from the sequence, we have developed high resolution FISH for visualization of mRNA distributions in whole animals. The high resolution and sensitivity afforded by the use of directly fluorescently labelled probes and confocal imaging permitted mRNA distributions to be recorded at the cellular and subcellular level. Expression patterns were obtained for 8 out of 10 genes in an initial test set of predicted gene sequences, indicating that FISH is an effective means of characterizing predicted genes in C. elegans.

L17 ANSWER 40 OF 50 MEDLINE DUPLICATE 30
ACCESSION NUMBER: 96042579 MEDLINE
DOCUMENT NUMBER: 96042579 PubMed ID: 7581455
TITLE: Developmental **expression pattern** screen for genes **predicted** in the C. elegans genome sequencing project.
AUTHOR: Lynch A S; Briggs D; Hope I A
CORPORATE SOURCE: Department of Pure and Applied Biology, University of Leeds, UK.
SOURCE: NATURE GENETICS, (1995 Nov) 11 (3) 309-13.
Journal code: 9216904. ISSN: 1061-4036.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951208

AB Maximum use should be made of information generated in the genome sequencing projects. Toward this end, we have initiated a genome sequence-based, **expression pattern** screen of genes **predicted** from the Caenorhabditis elegans genome sequence data. We examined beta-galactosidase expression patterns in C. elegans lines transformed with lacZ reporter gene fusions constructed using predicted C. elegans gene promoter regions. Of the predicted genes in the cosmids analysed so far, 67% are amenable to the approach and 54% of examined genes yielded a developmental expression pattern. Expression pattern information is being made generally available using computer databases.

L17 ANSWER 41 OF 50 MEDLINE DUPLICATE 31
ACCESSION NUMBER: 96432199 MEDLINE
DOCUMENT NUMBER: 96432199 PubMed ID: 8835265
TITLE: Cytokeratin 20 expression by non-invasive transitional cell carcinomas: potential for distinguishing recurrent from non-recurrent disease.
AUTHOR: Harnden P; Allam A; Joyce A D; Patel A; Selby P; Southgate J
CORPORATE SOURCE: Department of Histopathology, General Infirmary, Leeds, UK.
SOURCE: HISTOPATHOLOGY, (1995 Aug) 27 (2) 169-74.
Journal code: 7704136. ISSN: 0309-0167.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961204

AB Although approximately 50% of patients with non-invasive (Ta) papillary transitional cell carcinoma show no recurrence of their disease, current histopathological approaches cannot distinguish this sub-group from those patients in whom the disease will recur. In this 5 year retrospective study, we have shown that cytokeratin 20 (CK20) was expressed in 19 of 29 (65.5%) of non-invasive papillary tumours of grades 1 or 2. CK20 **expression patterns** were **predictive** of disease non-recurrence in a sub-group of eight patients, representing 51.7% of patients with non-recurrent disease. In normal bladder mucosa, CK20 expression was restricted to the terminally-differentiated superficial cell. In eight CK20-positive tumours which showed no recurrence at 5 years, CK20 expression was either restricted to, or most intense in, the luminal cells of the papillae. This pattern of expression was not seen in any of the 15 tumours from the recurrent group. Disruption of normal CK20 expression was highly significantly correlated with recurrent tumours. These results suggest that changes in the expression of differentiation-associated antigens, such as CK20, may be useful in predicting benign versus malignant behaviour and may, therefore, be useful in defining treatment strategies.

L17 ANSWER 42 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1995:221827 BIOSIS
DOCUMENT NUMBER: PREV199598236127
TITLE: Genetics of ecdysteroid-regulated central nervous system metamorphosis in Drosophila (Diptera: Drosophilidae.
AUTHOR(S): Restifo, Linda L. (1); Estes, Patricia S.; Russo, Christiana Dello
CORPORATE SOURCE: (1) ARL Div. Neurobiol., Univ. Arizona, Tucson, AZ 85721 USA
SOURCE: European Journal of Entomology, (1995) Vol. 92, No. 1, pp. 169-187.
ISSN: 1210-5759.
DOCUMENT TYPE: Article
LANGUAGE: English

AB We are interested in identifying members of the genetic pathway through which 20-hydroxyecdysone (20HE) mediates reorganization of the central nervous system (CNS) during metamorphosis. Our entry point is the Drosophila Broad-Complex (BR-C), an early 20HE-inducible locus with three genetic subfunctions, each represented by a lethal complementation group. Our previous analysis of mutants demonstrated that all three BR-C subfunctions are necessary for CNS morphogenesis and one is essential for visual system organization. We believe the mutant phenotypes result from faulty expression of genes normally regulated by the BRC family of zinc-finger proteins. BRC target genes are **predicted** to have **expression patterns** and/or mutant phenotypes that partially overlap with those of the BR-C. We have examined two candidate genes. IMP-E1 and Deformed (Dfd), to determine their positions relative to BR-C in the hormone-regulated pathway of CNS metamorphosis. Identified by Natzle and colleagues on the basis of 20HE-inducibility in imaginal discs, IMP-E1 transcripts were also found in a subset of CNS glial cells. Our recent experiments show that BR-C expression is spatially and temporally poised to regulate IMP-E1 induction by 20HE. We examined IMP-E1 transcript accumulation in larval and prepupal CNS of BR-C lethal mutants representing each of the three complementation groups. In all three cases, IMP-E1 induction in the CNS of BR-C mutants was comparable to that of wildtype and of genetic controls. Thus, activity of any individual BR-C subfunction is not essential for IMP-E1 induction. Dfd is a homeotic selector gene in the Antennapedia complex whose larval CNS expression has been shown by others to be restricted to a subset of subesophageal ganglion cells. We have demonstrated that Dfd mutants manifest a defect in subesophageal ganglion metamorphosis, namely separation from the thoracic ganglion, indistinguishable from that of BR-C mutants. However. Dfd transcript accumulation in the CNS appears to be indifferent to 20HE levels in vivo or in vitro. Alternative models for the genetic pathways controlling CNS metamorphosis are discussed.

L17 ANSWER 43 OF 50 MEDLINE DUPLICATE 32
ACCESSION NUMBER: 94355653 MEDLINE
DOCUMENT NUMBER: 94355653 PubMed ID: 8075397
TITLE: Wound-induced and developmental activation of a poplar tree chitinase gene promoter in transgenic tobacco.
AUTHOR: Clarke H R; Davis J M; Wilbert S M; Bradshaw H D Jr; Gordon M P

CORPORATE SOURCE: Department of Biochemistry, University of Washington, Seattle 98195.
SOURCE: PLANT MOLECULAR BIOLOGY, (1994 Aug) 25 (5) 799-815. Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U01660; GENBANK-U01661
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19941013
Last Updated on STN: 19941013
Entered Medline: 19940930

AB Wounding hybrid poplar (Populus trichocarpa x P. deltoides) trees results in the expression of novel wound-inducible (win) mRNAs thought to encode proteins involved in defense against pests and pathogens. Members of the win6 gene family encode acidic multi-domain chitinases, with combined structure and charge characteristics that differ from previously described chitinases. Win6 expression has been shown to occur in pooled unwounded leaves of a wounded (on multiple leaves) poplar plant. Here we demonstrate that wounding a single leaf induces win6 expression locally, in the wounded leaf, and remotely, in specific unwounded leaves with strong vascular connections to the wounded leaf. We also demonstrate that a win6 promoter-beta-glucuronidase (GUS) gene fusion (win6-GUS) responds to wounding locally and remotely in transgenic tobacco. These data indicate that the poplar win6 promoter has regulatory elements that are responsive to 'wound signals' in the heterologous host. In addition, win6-GUS is developmentally activated in unwounded young leaves and floral tissues of transgenic tobacco. Similar developmental expression patterns are found to occur for win6 in poplar trees, demonstrating that a herbaceous plant can serve as a host for woody tree transgene analysis and can accurately **predict expression patterns** in tree tissues (e.g. flowers) that would be difficult to study in free-living trees.

L17 ANSWER 44 OF 50 MEDLINE DUPLICATE 33
ACCESSION NUMBER: 94087232 MEDLINE
DOCUMENT NUMBER: 94087232 PubMed ID: 8263544
TITLE: Neuropeptide expression and processing as revealed by direct matrix-assisted laser desorption ionization mass spectrometry of single neurons.
AUTHOR: Jimenez C R; van Veelen P A; Li K W; Wildering W C; Geraerts W P; Tjaden U R; van der Greef J
CORPORATE SOURCE: Graduate School Neurosciences Amsterdam, Research Institute Neurosciences, Vrije Universiteit, Faculty of Biology, The Netherlands.
SOURCE: JOURNAL OF NEUROCHEMISTRY, (1994 Jan) 62 (1) 404-7. Journal code: 2985190R. ISSN: 0022-3042.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199401
ENTRY DATE: Entered STN: 19940209
Last Updated on STN: 19940209
Entered Medline: 19940124

AB Neuropeptides were directly detected in single identified neurons and the neurohemal area of peptidergic (neuroendocrine) systems in the Lymnaea

brain by using matrix-assisted laser desorption ionization mass spectrometry (MALDI-MS). The samples were placed in matrix solution and ruptured to allow mixing of cell contents with the matrix solution. After formation of matrix crystals, the analytes were analyzed by MALDI-MS. It was surprising that clean mass spectra were produced, displaying extreme sensitivity of detection. In one of the neuroendocrine systems studied, we could demonstrate for the first time, by comparing the peptide patterns of soma and of neurohemal axon terminals, that processing of the complex prohormone expressed in this system occurs entirely in the soma. In the other system studied, novel peptides could be detected in addition to peptides previously identified by conventional molecular biological and peptide chemical methods. Thus, complex peptide processing and **expression patterns** could be **predicted** that were not detected in earlier studies using conventional methods. As the first MALDI-MS study of direct peptide fingerprinting in the single neuron, these experiments demonstrate that MALDI-MS forms a new and valuable approach to the study of the synthesis and expression of bioactive peptides, with potential application to single-cell studies in vertebrates, including humans.

L17 ANSWER 45 OF 50 MEDLINE
ACCESSION NUMBER: 93313708 MEDLINE
DOCUMENT NUMBER: 93313708 PubMed ID: 8324639
TITLE: MacMatch: a tool for pattern-based protein secondary structure prediction.
AUTHOR: Presnell S R; Cohen B I; Cohen F E
CORPORATE SOURCE: Department of Pharmaceutical Chemistry, University of California-San Francisco 94143-0446.
SOURCE: COMPUTER APPLICATIONS IN THE BIOSCIENCES, (1993 Jun) 9 (3) 373-4.
Journal code: 8511758. ISSN: 0266-7061.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199308
ENTRY DATE: Entered STN: 19930820
Last Updated on STN: 19930820
Entered Medline: 19930810

AB A program is described for predicting the secondary structure of globular proteins on an Apple Macintosh computer. MacMatch produces turn **predictions** using augmented regular **expression** **pattern** matching. Helix and strand predictions are based on a neural network. Protein structural class (alpha/alpha), beta/beta, alpha/beta can be exploited to improve secondary structure prediction. The program is simple to use, and the package includes sets of tested patterns and trained neural networks.

L17 ANSWER 46 OF 50 MEDLINE DUPLICATE 34
ACCESSION NUMBER: 93162369 MEDLINE
DOCUMENT NUMBER: 93162369 PubMed ID: 1286772
TITLE: Regulation of Drosophila neural development by a putative secreted protein.
AUTHOR: Okano H; Hayashi S; Tanimura T; Sawamoto K; Yoshikawa S; Watanabe J; Iwasaki M; Hirose S; Mikoshiba K; Montell C
CORPORATE SOURCE: Department of Molecular Neurobiology, University of Tokyo, Japan.

SOURCE: DIFFERENTIATION, (1992 Dec) 52 (1) 1-11.
Journal code: 0401650. ISSN: 0301-4681.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L12697; GENBANK-L12698; GENBANK-L12699;
GENBANK-L12700; GENBANK-L12701; GENBANK-L12702;
GENBANK-L12703; GENBANK-S55367; GENBANK-X65506;
GENBANK-Z16406
ENTRY MONTH: 199303
ENTRY DATE: Entered STN: 19930402
Last Updated on STN: 19970203
Entered Medline: 19930318

AB The Drosophila strawberry (sty) locus was isolated by P-element insertion mutagenesis in a screen for mutations affecting eye development. Analysis of the mutant phenotype and the putative expression pattern of the sty gene suggested that it has multiple functions. Mutations in the sty gene lead to irregular spacing of ommatidia, an increase in the number of photoreceptor cells, as well as abnormal axonal projections to the lamina and disrupted structure of the optic lobes in the adult fly. The sty mutation also causes abnormal head involution, a change in a number of sensilla in the antennomaxillary complex in the embryonic stage and abnormal morphogenesis of the maxillary palp and wings in later stages. We examined the presumptive expression of the sty gene during development by histochemical staining for lacZ expression from enhancer trap elements inserted within the sty gene. During embryogenesis, expression of lacZ showed a segmental pattern in the ectoderm and in the nervous system. In the eye imaginal discs, lacZ was expressed in photoreceptor cells beginning a few rows posterior to the morphogenetic furrow. The lacZ was also expressed in the wing disc. In the adult, lacZ was expressed in the retina and lamina. We cloned the sty gene by P-element tagging and found that it encodes a putative secreted protein containing a cysteine-rich region similar to the epidermal growth factor (EGF) repeat. On the basis of the loss of functional phenotype, the **expression pattern** and the **predicted** structure of its product, we propose that sty encodes a diffusible protein acting as a signal involved in lateral inhibition within the developing nervous system and also as a factor involved either directly or indirectly in axonal guidance and optic lobe development.

L17 ANSWER 47 OF 50 MEDLINE DUPLICATE 35
ACCESSION NUMBER: 91115075 MEDLINE
DOCUMENT NUMBER: 91115075 PubMed ID: 2125959
TITLE: Isolation and expression of scabrous, a gene regulating neurogenesis in Drosophila.
AUTHOR: Mlodzik M; Baker N E; Rubin G M
CORPORATE SOURCE: Howard Hughes Medical Institute, University of California, Berkeley 94720.
SOURCE: GENES AND DEVELOPMENT, (1990 Nov) 4 (11) 1848-61.
Journal code: 8711660. ISSN: 0890-9369.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M37703; GENBANK-M60065
ENTRY MONTH: 199103
ENTRY DATE: Entered STN: 19910329
Last Updated on STN: 19970203

Entered Medline: 19910301

AB Mutations in the Drosophila scabrous (sca) gene affect eye and bristle development, leading to irregular spacing of ommatidia and bristle duplications in the adult fly. We have cloned the sca gene by P-element tagging. The sca transcription unit is 12 kb and consists of four exons that are joined in a 3.2-kb mRNA. In an enhancer trap screen we have isolated several P[lacZ] insertions close to the sca transcription start site. We have examined the expression pattern of sca by in situ hybridization to sca transcripts, by beta-galactosidase localization in the P[lacZ] lines, and by immunocytochemistry with an anti-sca antiserum. During embryogenesis, sca is expressed in a dynamic pattern associated with neural development. During imaginal development, sca is mainly expressed in the R8 photoreceptor precursor cells in the eye imaginal disc and in sensory organ precursor cells in other discs. In the wing disc, sca expression is coextensive with the anlagen for bristles and is controlled by genes of the achaete-scute complex. Based on its loss-of-function phenotype, **expression pattern**, and the **predicted** structure of its product, a secreted peptide with homology to the fibrinogen gene family, we propose that sca encodes a signal involved in lateral inhibition within individual domains of the developing nervous system.

L17 ANSWER 48 OF 50 MEDLINE DUPLICATE 36
ACCESSION NUMBER: 89356625 MEDLINE
DOCUMENT NUMBER: 89356625 PubMed ID: 2504582
TITLE: A novel spatial transcription pattern associated with the segmentation gene, giant, of Drosophila.
AUTHOR: Mohler J; Eldon E D; Pirrotta V
CORPORATE SOURCE: Department of Cell Biology, Baylor College of Medicine, Houston, TX 77030.
SOURCE: EMBO JOURNAL, (1989 May) 8 (5) 1539-48. Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198909
ENTRY DATE: Entered STN: 19900309 Last Updated on STN: 19970203 Entered Medline: 19890922

AB The segmentation gene, giant, is located in 3A1 within a cloned chromosome region surrounding the zeste locus. Rearrangement breakpoints associated with giant mutations were localized on the genomic clone map, and nearby transcription units were identified. One transcription unit is active during early embryogenesis and its transcripts are spatially localized from blastoderm into extended germband stages, consistent with expected **expression patterns predicted** by the 'gap' phenotype of giant mutants. Germ line transformation experiments using a 10-kb DNA fragment containing this transcription unit gave complete rescue of the abdominal giant defect but only partial correction of the head defect. The effect of mutations in three other gap loci, Kr, kni and hb, were also analyzed.

L17 ANSWER 49 OF 50 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:290056 BIOSIS
DOCUMENT NUMBER: BA88:15400
TITLE: UNUSUAL SEQUENCE OF AN ABSCISIC ACID-INDUCIBLE MESSENGER

RNA WHICH ACCUMULATES LATE IN BRASSICA-NAPUS SEED DEVELOPMENT.

AUTHOR(S): HARADA J J; DELISLE A J; BADEN C S; CROUCH M L
CORPORATE SOURCE: DEP. BOATNY, UNIV. CALIFORNIA, DAVIS, CALIF. 95616.
SOURCE: PLANT MOL BIOL, (1989) 12 (4), 395-402.
CODEN: PMBIDB. ISSN: 0167-4412.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB We have analyzed the nucleotide sequence and accumulation of an mRNA which is prevalent in seeds of Brassica napus L. During normal development, the mRNA begins to accumulate during late embryogeny, is stored in dry seeds, and becomes undetectable in seedlings within 24 hours after imbibition. Moreover, abscisic acid treatment of embryos precociously induces or enhances accumulation of the mRNA. Nucleotide sequencing studies how that the deduced 30 kDa polypeptide has an unusual primary structure; the polypeptide possesses direct amino acid sequence repeats and its virtually entirely hydrophilic with the exception of a hydrophobic carboxyl-terminal region. Based upon the **expression pattern** and **predicted** polypeptide sequence, we conclude that the mRNA is encoded by a late embryogenesis-abundant (Lea) gene in B. napus.

L17 ANSWER 50 OF 50 MEDLINE DUPLICATE 37

ACCESSION NUMBER: 89291517 MEDLINE
DOCUMENT NUMBER: 89291517 PubMed ID: 2472369
TITLE: Distribution of cytokeratin polypeptides in epithelia of the adult human urinary tract.
AUTHOR: Schaafsma H E; Ramaekers F C; van Muijen G N; Ooms E C; Ruiter D J
CORPORATE SOURCE: Department of Pathology, University Hospital Nijmegen, The Netherlands.
SOURCE: HISTOCHEMISTRY, (1989) 91 (2) 151-9.
Journal code: 0411300. ISSN: 0301-5564.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198908
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890803
AB Cytokeratin expression was studied in the epithelia lining the normal human urine conducting system using immunohistochemistry on frozen sections employing a panel of 14 monoclonal antibodies. Eleven of these anticytokeratin antibodies reacted specifically with one of the 19 human cytokeratin polypeptides. Profound differences were found in the cytokeratin expression patterns between the different types of epithelium in the male and female urinary tract. In the areas showing morphological transitions of transitional epithelium to columnar epithelium and of nonkeratinizing squamous epithelium to keratinizing squamous epithelium gradual shifts of cytokeratin **expression patterns** were observed, often **anticipating** the morphological changes. However, also within one type of epithelium, i.e. the transitional epithelium, two different patterns of cytokeratin expression were found. Expression of cytokeratin 7 was homogeneous in the transitional epithelium of renal pelvis and ureter but heterogeneous in the transitional epithelium of the bladder. Furthermore, intraepithelial differences in cytokeratin expression could be shown to be differentiation related. Using a panel of chain-specific monoclonal antibodies to cytokeratins 8 and 18

conformational and/or biochemical changes in the organization of these intermediate filaments were demonstrated upon differentiation in columnar and transitional epithelium.

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=> d history

     (FILE 'HOME' ENTERED AT 11:50:48 ON 09 JUL 2002)

     FILE 'MEDLINE, BIOSIS' ENTERED AT 11:51:25 ON 09 JUL 2002
L1         14581 S EST# OR (SEQUENCE(W)TAG#)
L2            83 S L1(S)("NOT" OR CANNOT)
L3            55 DUP REM L2 (28 DUPLICATES REMOVED)
L4         13496 S EST OR ESTS OR (SEQUENCE(W)TAG#)
L5            83 S L2 (S)("NOT" OR CANNOT)
L6            82 S L4 (S)("NOT" OR CANNOT)
L7       1637565 S MRNA OR CDNA OR POLYNUCLEOTIDE# OR DNA OR TRANSCRIPT#
L8        544939 S MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#
L9         11399 S L8(S)(EXPRESSION(W)PATTERN#)
L10           90 S L9(S)(CANNOT OR "NOT")
L11           51 DUP REM L10 (39 DUPLICATES REMOVED)
L12        28138 S (EXPRESSION(A)PATTERN#)
L13          110 S L12(5A)(PREDICT? OR ANTICIPAT?)
L14           12 S L13 AND DATABASE#
L15            7 DUP REM L14 (5 DUPLICATES REMOVED)
L16           87 S L12(3A)(PREDICT? OR ANTICIPAT?)
L17           50 DUP REM L16 (37 DUPLICATES REMOVED)

=> s l12(s)splic?
L18         1201 L12(S) SPLIC?

=> s l18(s)l1
L19           23 L18(S) L1

=> dup rem l19
PROCESSING COMPLETED FOR L19
L20           13 DUP REM L19 (10 DUPLICATES REMOVED)

=> d ibib abs tot

L20  ANSWER 1 OF 13     MEDLINE                              DUPLICATE 1
ACCESSION NUMBER:    2002004295     MEDLINE
DOCUMENT NUMBER:     21624819   PubMed ID: 11752299
TITLE:               The Gene Resource Locator: gene locus maps for
                     transcriptome analysis.
AUTHOR:              Honkura Toshihiko; Ogasawara Jun; Yamada Tomoyuki;
                     Morishita Shinichi
CORPORATE SOURCE:    Department of Complexity Science and Engineering, Faculty
                     of Frontier Science, University of Tokyo, 7-3-1 Hongo,
                     Bunkyo-ku, Tokyo 113-0033, Japan.
SOURCE:              NUCLEIC ACIDS RESEARCH, (2002 Jan 1) 30 (1) 221-5.
                     Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY:        England: United Kingdom
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         200201
ENTRY DATE:          Entered STN: 20020102
                     Last Updated on STN: 20020125
                     Entered Medline: 20020121
AB   Since the advent of the draft human genome sequence there has been
growing
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interest in transcriptome analysis based on genomic data. The Gene Resource Locator (GRL) assembles gene maps that include information on gene-**expression patterns**, cis-elements in regulatory regions and alternatively **spliced** transcripts. The database was constructed using customized software, and currently contains 2.2 million alignments (exon-intron structures). The alignments have been annotated and integrated into a system that encompasses approximately 90 000 **EST** loci sharing common exons, 8091 alternatively **spliced** transcript groups, 10 801 expression-profile groups, 8066 candidate regulatory regions in full-length cDNAs, and 1 million SNP loci. We have used Flash technology to build a dynamic web viewer that facilitates browsing through the millions of alignments. All of the information is available through the World Wide Web at the Gene Resource Locator web site (http://grl.gi.k.u-tokyo.ac.jp).

L20 ANSWER 2 OF 13 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001700169 MEDLINE
DOCUMENT NUMBER: 21615301 PubMed ID: 11748642
TITLE: Gene expression patterns in melanocytic cells: candidate markers for early stage and malignant transformation.
AUTHOR: Meije Clifton B; Hakvoort Theodorus B M; Swart Guido W M; Westerhof Wiete; Lamers Wouter H; Das Pranab K
CORPORATE SOURCE: Department of Pathology, Academic Medical Center, University of Amsterdam, The Netherlands.
SOURCE: JOURNAL OF PATHOLOGY, (2002 Jan) 196 (1) 51-8. Journal code: 0204634. ISSN: 0022-3417.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011219
Last Updated on STN: 20020205
Entered Medline: 20020204

AB Different stages of differentiation of human melanocytic cells, such as normal melanocytes, naevus and melanoma cells, reflect distinct gene **expression patterns**. A PCR-based subtractive hybridization and display method was applied to identify genes that are differentially expressed in melanocytic cells in relation to early stage and malignant transformation. This resulted in the identification of a number of candidate cDNAs differentially expressed among melanocytes, naevus cells, and (non)-metastatic melanoma cells. Out of this collection of cDNAs, 16 clones were screened that comprised 12 novel genes, one previously identified expressed **sequence tag** related to vesicular trafficking (Ras-related protein Rab5b). The other three were also known genes that were either related to cell motility (beta-tubulin), pre-mRNA **splicing** (small nuclear protein U1A), or of unknown function (the human TI227-H gene). The differential **expression patterns** of Rab5b and two novel gene fragments (pCMa1, pCMn2) were further assessed in melanocytic cells. pCMa1 was expressed more in metastatic melanoma than in primary melanoma cells. In contrast, pCMn2 was expressed in both non-metastatic and metastatic melanoma cells, but was not detectable in either normal melanocytes or naevus cells. The Ras-related protein Rab5b showed lower levels of expression in highly metastatic than in other melanoma cells. These three cDNAs may therefore be involved in the early stage and malignant transformation of melanocytes.

L20 ANSWER 3 OF 13 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:372790 BIOSIS
DOCUMENT NUMBER: PREV200200372790
TITLE: Cloning and characterization of human ubiquitin binding enzyme 2 cDNA.
AUTHOR(S): Li Guangtao; Lu Hongyan; Zhou Yan; Jin Jian; Jiang Keyi; Peng Xiaozhong; Yuan Jiangang (1); Qiang Boqin
CORPORATE SOURCE: (1) National Laboratory of Medical Molecular Biology, Institute of Basic Medical Sciences, CAMS and PUMC, Chinese National Human Genome Center, Beijing, 100005 China
SOURCE: Chinese Medical Sciences Journal, (March, 2002) Vol. 17, No. 1, pp. 7-12. print.
ISSN: 1001-9294.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Objective: To clone and identify the gene encoding human ubiquitin binding enzyme 2 and study its **expression pattern**. Methods: According to the sequence of human **EST**, which is highly homologous to the mouse ubiquitin binding/conjugating enzyme (E2), primers were synthesized to screen the human fetal brain cDNA library. The gene was analyzed by bioinformatics technique and its **expression pattern** was studied by using multiple-tissue Northern blot. Results: Two cDNA clones encoding human ubiquitin conjugating enzyme have been isolated and identified. Both containing the ubiquitin conjugating domain, the 2 cDNA clones are 88% identical in amino acid sequences and **splicing** isoforms to each other only with an exon excised to form the short sequence. They belong to a highly conserved and widely expressed E2 enzyme family. Northern blot shows that they are expressed exclusively in adult human heart, placenta, and pancreas but no transcripts can be detected in brain, lung, liver, skeletal muscle or kidney. Conclusions: The gene encoding human ubiquitin binding enzyme is expressed under temporal control. As a key enzyme in the degradation of proteins, ubiquitin conjugating enzymes play a central role in the expression regulation on the level of post-translation.

L20 ANSWER 4 OF 13 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001314104 MEDLINE
DOCUMENT NUMBER: 21280915 PubMed ID: 11386757
TITLE: Central nervous system, uterus, heart, and leukocyte expression of the LOXL3 gene, encoding a novel lysyl oxidase-like protein.
AUTHOR: Jourdan-Le Saux C; Tomsche A; Ujfalusi A; Jia L; Csiszar K
CORPORATE SOURCE: Pacific Biomedical Research Center, University of Hawaii, 1993 East-West Road, Honolulu, Hawaii, 96822.
CONTRACT NUMBER: CA76580 (NCI)
RR03061 (NCRR)
SOURCE: GENOMICS, (2001 Jun 1) 74 (2) 211-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA852888; GENBANK-AF311313; GENBANK-AI752772; GENBANK-R55706
ENTRY MONTH: 200110

ENTRY DATE: Entered STN: 20011008
Last Updated on STN: 20011008
Entered Medline: 20011004

AB A BLASTN search using the mouse lor-2 cDNA identified three overlapping **ESTs** (AI752772, AA852888, and R55706) in the GenBank database. These expressed **sequence tags** were assembled into a contig of 3121 nucleotides with an open reading frame of 2262 bp. The encoded putative polypeptide of 754 amino acids presented all structural characteristics of the lysyl oxidase (LOX) enzyme family, a copper-binding site with four histidyl residues, the lysyl and tyrosyl residues known to be involved in LOX enzyme in the formation of the quinone cofactor and surrounding sequences, and the cytokine receptor-like domain. In addition, four scavenger receptor cysteine-rich (SRCR) domains were found in the N-terminal region of the protein. The gene encoding this new cDNA, which we have referred to as human lysyl oxidase-like 3 (humanLOXL3), has been mapped to chromosome 2p13.3, overlapping at its 3' end the HtrA2 serine protease gene. The structure of the humanLOXL3 gene was deduced from the BAC clone bac91a19 sequence and contained 14 exons. The **expression pattern** of this new member of the LOX gene family appears to be different from that of the LOX and LOX-like genes, as the central nervous system, neurons, and also leukocytes expressed humanLOXL3. A BLASTN search of the human **EST** database indicated the presence of **ESTs** , corresponding to alternative **splice** variants of LOXL3, that lacked exon 5 and exon 8. The putative resulting protein retained the region encoding the structural and functional elements of the amine oxidase but the second and fourth SRCR domains were truncated and the potential BMP-1 cleavage site was not present. The presence of domains unrelated to the traditional amine oxidase activity is a strong indication that humanLOXL3 might fulfill other functions in addition to intrinsic enzyme activity.

L20 ANSWER 5 OF 13 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2001297501 MEDLINE
DOCUMENT NUMBER: 21272509 PubMed ID: 11376952
TITLE: The cloning, genomic structure, localization, and expression of human deoxyribonuclease IIbeta.
AUTHOR: Krieser R J; MacLea K S; Park J P; Eastman A
CORPORATE SOURCE: Department of Pharmacology and Toxicology, Dartmouth Medical School, 7650 Remsen, Hanover, NH 03755, USA.
CONTRACT NUMBER: CA23108 (NCI)
CA50224 (NCI)
SOURCE: GENE, (2001 May 16) 269 (1-2) 205-16.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF274571
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

AB Acidic endonuclease activity is present in all cells in the body and much of this can be attributed to the previously cloned and ubiquitously expressed deoxyribonuclease II (DNase II). Database analysis revealed the existence of expressed **sequence tags** and genomic

segments coding for a protein with considerable homology to DNase II. This report describes the cloning of this cDNA, which we term deoxyribonuclease IIbeta (DNase IIbeta) and comparison of its expression to that of the originally cloned DNase II (now termed DNase IIalpha). The cDNA encodes a 357 amino acid protein. This protein exhibits extensive homology to DNase IIalpha including an amino-terminal signal peptide and a conserved active site, and has many of the regions of identity that are conserved in homologs in other mammals as well as C. elegans and Drosophila. The gene encoding DNase IIbeta has identical **splice** sites to DNase IIalpha. Human DNase IIbeta is highly expressed in the salivary gland, and at low levels in trachea, lung, prostate, lymph node, and testis, whereas DNase IIalpha is ubiquitously expressed in all tissues. The **expression pattern** of human DNase IIbeta suggests that it may function primarily as a secreted enzyme. Human saliva was found to contain DNase IIalpha, but after immunodepletion, considerable acid-active endonuclease remained which we presume is DNase IIbeta. We have localized the gene for human DNase IIbeta to chromosome 1p22.3 adjacent (and in opposing orientation) to the human uricase pseudogene. Interestingly, murine DNase IIbeta is highly expressed in the liver. Uricase is also highly expressed in mouse but not human liver and this may explain the difference in **expression patterns** between human and mouse DNase IIbeta.

L20 ANSWER 6 OF 13 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2001676977 MEDLINE
DOCUMENT NUMBER: 21579789 PubMed ID: 11722847
TITLE: Genomic organization and expression profile of the parvin family of focal adhesion proteins in mice and humans.
AUTHOR: Korenbaum E; Olski T M; Noegel A A
CORPORATE SOURCE: Institute for Biochemistry I, Medical Faculty, University of Cologne, Joseph-Stelzmann-Strasse 52, 50931, Cologne, Germany.. elena.korenbaum@uni-koeln.de
SOURCE: GENE, (2001 Nov 14) 279 (1) 69-79.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011128
Last Updated on STN: 20020125
Entered Medline: 20020116

AB We have characterized the genomic organization and the **expression pattern** of alpha-, beta- and gamma-parvin, a novel family of focal adhesion proteins, in mice and humans. alpha-Parvin is nearly ubiquitously expressed, beta-parvin is preferentially expressed in heart- and skeletal muscle, and gamma-parvin in lymphoid tissues. Parvins display diverse patterns of developmental regulation. The alpha-form is present throughout mouse development, beta-parvin is gradually upregulated and gamma-parvin is downregulated at embryonic day 11. The human alpha-parvin gene (PARVA), extending over 160 kb, is located on chromosome 11. Both, the human beta-parvin gene (PARVB), which is over 145 kb long, and the gamma-parvin gene (PARVG) of a total length of about 25 kb are positioned on chromosome

22 with PARVG located about 12 kb downstream of the 3' end of PARVB. Multiple tissue array analysis indicates that parvins are expressed at reduced levels in cancer as compared to the corresponding normal tissues. Analysis of **ESTs** and PCR-amplified fragments reveals alternatively **spliced** and alternatively polyadenylated gene products. Mammalian parvins are likely to have arisen late in evolution from gene duplication as they share a remarkably similar exon/intron organization, which is different from the organization of the single genes encoding parvin-like proteins in Drosophila and Caenorhabditis.

L20 ANSWER 7 OF 13 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2001654641 MEDLINE
DOCUMENT NUMBER: 21564202 PubMed ID: 11707072
TITLE: From PREDs and open reading frames to cDNA isolation: revisiting the human chromosome 21 transcription map.
AUTHOR: Reymond A; Friedli M; Henrichsen C N; Chapot F; Deutsch S; Ucla C; Rossier C; Lyle R; Guipponi M; Antonarakis S E
CORPORATE SOURCE: Division of Medical Genetics, University of Geneva Medical School, Geneva, 1211, Switzerland.
SOURCE: GENOMICS, (2001 Nov) 78 (1-2) 46-54.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF358257; GENBANK-AF358258; GENBANK-AF360358; GENBANK-AF363446; GENBANK-AF363447; GENBANK-AF375989; GENBANK-AF380178; GENBANK-AF380179; GENBANK-AF380180; GENBANK-AF380181; GENBANK-AF380182; GENBANK-AF380183; GENBANK-AF380184; GENBANK-AF391112; GENBANK-AF391113; GENBANK-AF391114; GENBANK-AF391115; GENBANK-AJ409094; GENBANK-AY033899; GENBANK-AY033900; GENBANK-AY033901; GENBANK-AY033902; GENBANK-AY033903; GENBANK-AY033904; GENBANK-AY033905; GENBANK-AY033906; GENBANK-AY033907; GENBANK-AY033908; GENBANK-AY035381; GENBANK-AY035382; GENBANK-AY035383; GENBANK-AY037804; GENBANK-AY039243; GENBANK-AY039244; GENBANK-AY040086; GENBANK-AY040087; GENBANK-AY040088; GENBANK-AY040089; GENBANK-AY040090; GENBANK-AY040873; GENBANK-AY040874; GENBANK-AY040875; GENBANK-AY040876
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011115
Last Updated on STN: 20020125
Entered Medline: 20020107

AB A supernumerary copy of human chromosome 21 (HC21) causes Down syndrome. To understand the molecular pathogenesis of Down syndrome, it is necessary to identify all HC21 genes. The first annotation of the sequence of 21q confirmed 127 genes, and predicted an additional 98 previously unknown "anonymous" genes (predictions (PREDs) and open reading frames (C21orfs)), which were foreseen by exon prediction programs and/or **spliced** expressed **sequence tags**. These putative gene models still need to be confirmed as bona fide transcripts. Here we report the characterization and **expression pattern** of the putative transcripts C21orf7, C21orf11, C21orf15, C21orf18, C21orf19, C21orf22, C21orf42, C21orf50, C21orf51, C21orf57, and C21orf58, the GC-rich sequence DNA-binding factor candidate GCFC (also known as C21orf66), PRED12, PRED31, PRED34, PRED44, PRED54, and PRED56. Our analysis showed that most of the C21orfs originally defined by matching

spliced expressed **sequence tags** were correctly predicted, whereas many of the PREDs, defined solely by computer prediction, do not correspond to genuine genes. Four of the six PREDs were incorrectly predicted: PRED44 and C21orf11 are portions of the same transcript, PRED31 is a pseudogene, and PRED54 and PRED56 were wrongly predicted. In contrast, PRED12 (now called C21orf68) and PRED34 (C21orf63) are now confirmed transcripts. We identified three new genes, C21orf67, C21orf69, and C21orf70, not previously predicted by any programs. This revision of the HC21 transcriptome has consequences for the entire genome regarding the quality of previous annotations and the total number of transcripts. It also provides new candidates for genes involved in Down syndrome and other genetic disorders that map to HC21.

L20 ANSWER 8 OF 13 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2002047669 MEDLINE
DOCUMENT NUMBER: 21632271 PubMed ID: 11775832
TITLE: Biological function of a novel gene overexpressed in human hepatocellular carcinoma.
AUTHOR: Liu J; Zhou R; Zhang N; Rui J; Jin C
CORPORATE SOURCE: Department of Cell Biology, Beijing Medical University, Beijing 100083, China.
SOURCE: CHINESE MEDICAL JOURNAL, (2000 Oct) 113 (10) 881-5. Journal code: 7513795. ISSN: 0366-6999.
PUB. COUNTRY: China
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020215
Entered Medline: 20020214

AB OBJECTIVE: To clone the full-length of a differentially expressed cDNA fragment, LC27, and study its biological function tentatively. METHODS: Northern blot was used to analyze the **expression pattern** of LC27 in hepatocellular carcinoma, matched nontumor liver tissues, fetal liver and normal adult liver tissues, as well as BEL-7402 hepatocellular carcinoma cell line **ESTs splicing** and 5' rapid amplification of cDNA ends (5' RACE) were used to clone the full-length of LC27 cDNA. An antisense oligodeoxynucleotide approach was used to investigate the biological role of the gene in the proliferation of BEL-7402 cells. RESULTS: A 2186 bp novel cDNA with an open reading frame encoding a 283 amino acid protein was cloned. Analysis of the deduced amino acid sequence indicated that it is 38% (88/229) identical to human Golgi 4-transmembrane spanning transporter MTP. The gene and the encoded protein was termed hepatocellular carcinoma overexpressed transmembrane protein (hotp) and HOTP, respectively. Hotp mRNA was almost undetectable in normal adult liver and fetal liver tissues. However, it was significantly up-regulated in hepatocellular carcinoma and some matched nontumor liver tissues, as well as BEL-7402 cells. The proliferation of BEL-7402 cells was suppressed by an antisense oligodeoxynucleotide against hotp mRNA at a concentration of 50 micrograms/ml. CONCLUSION: HOTP may be an integral membrane transporter protein. The overexpression of the gene in hepatocellular carcinoma may play an important role in hepatocarcinogenesis and disease progression.

L20 ANSWER 9 OF 13 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:311677 BIOSIS
DOCUMENT NUMBER: PREV200100311677
TITLE: Identification of thrombopoietin specific genes by gene chip analysis.
AUTHOR(S): Vij, Ravi (1); Watson, Mark; Ritchey, Julie (1); Yang, Jianing (1); Holt, Matthew (1); Haug, Jeffrey (1); DiPersio, John (1)
CORPORATE SOURCE: (1) Division of BMT and Stem Cell Biology, Washington University School of Medicine, St. Louis, MO USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 288a. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB To date despite utilization of a variety of molecular techniques no cytokine specific genes have been identified. This has led several investigators to conclude that perhaps cytokine signalling through their receptors plays only a permissive role in hematopoiesis and cell fate during differentiation is predetermined. We have utilized microarray technology to address the stochastic vs deterministic role of cytokine receptors in thrombopoiesis. We have transfected murine BAF/3 cell lines which possess an endogeneous mIL-3 receptor with the receptor for human thrombopoietin (c-mpl) and various truncations of the human c-mpl receptor. BAF/3 cells transfected with the full length hmpl receptor were cultured in media containing RPMI 1640+ 10%fetal calf serum +1%L-Glutamine+ 1%Penicillin/Streptomycin and stimulated with either mIL-3 (5ng/ml) or human thrombopoietin (hTPO)(50ng/ml) or a combination of the two cytokines for a period of 24 hours. RNA was extracted, cRNA was prepared and hybridized to Affemetrix Gene Chips containing 11,000 known mouse genes and **ESTs** on two chips. A preliminary analysis of the data has revealed that stimulation with hTPO resulted in a definite three fold overexpression of 94 genes+**ESTs** compared to mIL-3 alone with transcripts for 56 of these genes+**ESTs** being detected only in cells stimulated with hTPO.5 known genes were upregulated > 5 fold after stimulation with TPO (Ataxia Telengectasia gene homolog, epididymal glycoprotein, T cell specific CCDI, early T lymphocyte activation protein and osteopontin). Stimulation with mIL3+hTPO resulted in > 3 fold overexpression of 175 genes+**ESTs** when compared to mIL3 with 83 being specifically induced by mIL3+hTPO. Transcripts for 3 known genes were detected only after stimulation with mIL3+hTPO (cyclin C, PS2, TCOF1). In addition expression of 8 other known genes were upregulated > 5 fold (zinc finger protein MOK2, p53 variant, fatty acid synthetase, ubiquitin carboxy-terminal hydrolase, **splicing** factor U2F, ribosomal protein S12, non muscle tropomyosin 5 and ASF). We are currently in the process of performing a detailed analysis of the overall gene **expression patterns** and conducting time course experiments using the cells transfected with human c-mpl and analyzing cells transfected with truncations of the human c-mpl receptor.

ACCESSION NUMBER: 2001:519168 BIOSIS
DOCUMENT NUMBER: PREV200100519168
TITLE: DNA chips designed to detect alternative splicing using LEADS.

AUTHOR(S): Wasserman, Alon (1); Shoshan, Avi (1); Grebinskiy, Vladimir
(1)
CORPORATE SOURCE: (1) Compugen Inc., Jamesburg, NJ USA
SOURCE: International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 63. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference Miami Beach, Florida, USA September 12-15, 2000
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We design chips enabling the detection of alternative **splice** variants. The design optimally chooses segments representing the **splice** variants of each gene. Probes are selected from each segment using criteria including specificity, distance from the 3' end, sequence quality, GC content, and so on. The designs are based on the LEADS software that clusters and assembles **ESTs**, known mRNAs and genomic data. For each gene, it produces a list of predicted mRNA transcripts, each a different **splice** variant. Multiply covered areas are used to detect and eliminate sequencing errors. These areas are also used for the detection of polymorphisms, which can be used in genotyping chips. Having good designs is crucial to extract meaningful information from chip experiments. Designs not using all available data, **splice** variants and sequencing errors might lead to useless probes and misleading results. It is believed that at least 35% of human genes have alternative **splice** variants, and it is important to distinguish between their **expression patterns**. This is achieved by choosing probes that are unique to some of the variants. If one just wishes to measure the overall expression level of the gene, probes that are common to all the variants can be chosen.

L20 ANSWER 11 OF 13 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2000082975 MEDLINE
DOCUMENT NUMBER: 20082975 PubMed ID: 10613851
TITLE: Frequent alternative splicing of human genes.
AUTHOR: Mironov A A; Fickett J W; Gelfand M S
CORPORATE SOURCE: State Center of Biotechnology NIIGenetika, Moscow, 113545, Russia.
SOURCE: GENOME RESEARCH, (1999 Dec) 9 (12) 1288-93.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000204
Last Updated on STN: 20000204
Entered Medline: 20000127

AB Alternative **splicing** can produce variant proteins and **expression patterns** as different as the products of different genes, yet the prevalence of alternative **splicing** has not been quantified. Here the **spliced** alignment algorithm was used to make a first inventory of exon-intron structures of known human genes using **EST** contigs from the TIGR Human Gene Index. The results on any one gene may be incomplete and will require verification, yet the overall trends are significant. Evidence of alternative **splicing** was shown in 35% of genes and the majority of **splicing** events occurred in 5' untranslated regions, suggesting wide occurrence of alternative regulation. Most of the alternative **splices** of coding regions generated additional protein domains

rather than alternating domains.

L20 ANSWER 12 OF 13 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 1998234549 MEDLINE
DOCUMENT NUMBER: 98234549 PubMed ID: 9570954
TITLE: Identification, characterization, and genetic mapping of Rad51d, a new mouse and human RAD51/RecA-related gene.
AUTHOR: Pittman D L; Weinberg L R; Schimenti J C
CORPORATE SOURCE: Jackson Laboratory, Bar Harbor, Maine 04609, USA.
CONTRACT NUMBER: CA34196 (NCI)
GM45415 (NIGMS)
HD07065 (NICHD)
+
SOURCE: GENOMICS, (1998 Apr 1) 49 (1) 103-11.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF034955; GENBANK-AF034956
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 19980708
Entered Medline: 19980625

AB Homologous DNA recombination occurs in all organisms and is important for repair of DNA damage during mitosis. One of the critical genes for DNA repair and meiotic recombination in yeast is RAD51, and homologs of RAD51 have been identified in several species, including mouse and human. Here we describe a new RAD51-related mammalian gene, named Rad51d, identified by searching the **EST** database with the yeast RAD55 and human RAD51B/REC2 genes. A full-length 1.5-kb mouse cDNA clone that encodes a predicted 329-amino-acid protein was isolated. Rad51d mRNA was present in every mouse tissue examined. Four different transcript sizes were detected, one of which was specific to testis. Human cDNA clones that predicted 71% amino acid identity to the mouse protein were also isolated.

Interestingly, the sequences of these human clones and of RT-PCR-derived products provided evidence for alternative **splicing**. These mRNAs are predicted to encode proteins that are truncated relative to the mouse and lack the ATP-binding motif characteristic of RecA-related proteins. Using an interspecific backcross mapping panel, Rad51d was mapped to mouse Chromosome 11, 48.5 cM from the centromere. By radiation hybrid mapping, the human ortholog RAD51D was mapped to chromosome 17q11, which is a region syntenic to mouse Chromosome 11. Due to its **expression pattern** and sequence similarity to other RAD51 family members, it is likely that Rad51d is part of a complex of proteins required for DNA repair and meiotic recombination.

L20 ANSWER 13 OF 13 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 97432815 MEDLINE
DOCUMENT NUMBER: 97432815 PubMed ID: 9286695
TITLE: Genomic organization of two novel genes on human Xq28: compact head to head arrangement of IDH gamma and TRAP delta is conserved in rat and mouse.
AUTHOR: Brenner V; Nyakatura G; Rosenthal A; Platzer M
CORPORATE SOURCE: Institut fur Molekulare Biotechnologie, Jena, Germany.
SOURCE: GENOMICS, (1997 Aug 15) 44 (1) 8-14.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U52111; GENBANK-U52112; GENBANK-U63009; GENBANK-U68564; GENBANK-U69268; GENBANK-U69269; GENBANK-U73205; GENBANK-Z68907; GENBANK-Z69043
ENTRY MONTH: 199711
ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 19990129
Entered Medline: 19971118

AB In this paper we present the entire genomic sequence as well as the cDNA sequence of two new human genes encoding the gamma subunit of the NAD(+)-dependent isocitrate dehydrogenase (H-IDH gamma) and the translocon-associated protein delta subunit (TRAP delta). These genes are located on region q28 of the human X chromosome, approximately 70 kb telomeric to the adrenoleukodystrophy locus (ALD). The sequences of the transcripts of both genes were obtained by searching the **EST** database with genomic data. Identified **ESTs** were completely sequenced and assembled to cDNAs comprising the entire coding region. For IDH gamma, several **EST** clones indicate differential **splicing**. IDH gamma and TRAP delta are arranged in a compact head to head manner. The nontranscribed intergenic region represents only 133 bp and is embedded in a CpG island. The CpG island obviously functions as a bidirectional promoter to initiate the transcription of both functionally unrelated genes with quite distinct **expression patterns**. This exceptional gene arrangement prompted us to clone and sequence genomic DNA fragments containing the homologous intergenic regions of rat and mouse. We show that in both species this area is similarly compact and represents less than 249 bp in rat and not more than 164 bp in mouse. In both cases this intergenic region is embedded in a CpG island and is highly conserved with nucleotide identity values ranging from 70.1% between human and rat to 92.6% between mouse and rat.

=> d history

(FILE 'HOME' ENTERED AT 11:50:48 ON 09 JUL 2002)

FILE 'MEDLINE, BIOSIS' ENTERED AT 11:51:25 ON 09 JUL 2002 .

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L2           83 S L1(S)("NOT" OR CANNOT)
L3           55 DUP REM L2 (28 DUPLICATES REMOVED)
L4        13496 S EST OR ESTS OR (SEQUENCE(W)TAG#)
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L6           82 S L4 (S)("NOT" OR CANNOT)
L7      1637565 S MRNA OR CDNA OR POLYNUCLEOTIDE# OR DNA OR TRANSCRIPT#
L8       544939 S MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#
L9        11399 S L8(S)(EXPRESSION(W)PATTERN#)
L10          90 S L9(S)(CANNOT OR "NOT")
L11          51 DUP REM L10 (39 DUPLICATES REMOVED)
L12       28138 S (EXPRESSION(A)PATTERN#)
L13         110 S L12(5A)(PREDICT? OR ANTICIPAT?)
L14          12 S L13 AND DATABASE#
L15           7 DUP REM L14 (5 DUPLICATES REMOVED)
L16          87 S L12(3A)(PREDICT? OR ANTICIPAT?)
L17          50 DUP REM L16 (37 DUPLICATES REMOVED)
L18        1201 S L12(S)SPLIC?
L19          23 S L18(S)L1
L20          13 DUP REM L19 (10 DUPLICATES REMOVED)
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=> s database#(3a)(rely or relied)
L21          41 DATABASE#(3A)(RELY OR RELIED)

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L22           0 L21(S) L12

=> s database#(3a)(establish?)
L23         871 DATABASE#(3A)(ESTABLISH?)

=> s l23(s)l12
L24           5 L23(S) L12

=> dup rem l24
PROCESSING COMPLETED FOR L24
L25           3 DUP REM L24 (2 DUPLICATES REMOVED)

=> d ibib abs tot

L25  ANSWER 1 OF 3     MEDLINE                              DUPLICATE 1
ACCESSION NUMBER:    2001020820     MEDLINE
DOCUMENT NUMBER:     20326781   PubMed ID: 10870966
TITLE:               Two-dimensional electrophoresis map of the human
                     hepatocellular carcinoma cell line, HCC-M, and
                     identification of the separated proteins by mass
                     spectrometry.
AUTHOR:              Seow T K; Ong S E; Liang R C; Ren E C; Chan L; Ou K; Chung
                     M C
CORPORATE SOURCE:    Bioprocessing Technology Center, National University of
                     Singapore, Singapore.
SOURCE:              ELECTROPHORESIS, (2000 May) 21 (9) 1787-813.
                     Journal code: 8204476. ISSN: 0173-0835.
PUB. COUNTRY:        GERMANY: Germany, Federal Republic of
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         200011
ENTRY DATE:          Entered STN: 20010322
                     Last Updated on STN: 20010322
                     Entered Medline: 20001103
AB   Currently, one of the most popular applications of proteomics is in the
     area of cancer research. In Africa, Southeast Asia, and China,
     hepatocellular carcinoma is one of the most common cancers, occurring as
     one of the top five cancers in frequency. This project was initiated with
     the purpose of separating and identifying the proteins of a human
     hepatocellular carcinoma cell line, HCC-M. After two-dimensional gel
     electrophoresis separation, silver staining, matrix-assisted laser
     desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS)
     analyses, tryptic peptide masses were searched for matches in the
     SWISS-PROT and NCBI nonredundant databases. Approximately 400 spots were
     analyzed using this approach. Among the proteins identified were
     housekeeping proteins such as alcohol dehydrogenase, alpha-enolase,
     asparagine synthetase, isocitrate dehydrogenase, and glucose-6-phosphate
     1-dehydrogenase. In addition, we also identified proteins with
     expression patterns that have been postulated to be
     related to the process of carcinogenesis. These include 14-3-3 protein,
     annexin, prohibitin, and thioredoxin peroxidase. This study of the HCC-M
     proteome, coupled with similar proteome analyses of normal liver tissues,
     tumors, and other hepatocellular carcinoma cell lines, represents the
     first step towards the establishment of protein
     databases, which are valuable resources in studies on the
     differential protein expressions of human hepatocellular carcinoma.
```

L25 ANSWER 2 OF 3 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2000498085 MEDLINE
DOCUMENT NUMBER: 20398317 PubMed ID: 10938339
TITLE: High throughput cellular localization of specific plant mRNAs by liquid-phase in situ reverse transcription-polymerase chain reaction of tissue sections.
AUTHOR: Koltai H; Bird D M
CORPORATE SOURCE: Department of Plant Pathology, North Carolina State University, Raleigh, North Carolina 27695, USA.
SOURCE: PLANT PHYSIOLOGY, (2000 Aug) 123 (4) 1203-12.
Journal code: 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027
Entered Medline: 20001018

AB Advances in high throughput DNA sequencing and bioinformatic gene discovery far outpace our ability to analyze gene function, necessitating development of more efficient means to examine expression at the cellular level. Here we present a polymerase chain reaction-based method to detect mRNA species in situ in which essentially all of the steps are carried out in liquid phase in a 96-well microtiter tray and only the final signal detection is performed on a microscope slide. We demonstrate the sensitivity of the method by the cellular localization of mRNA for the Tkn2 transcription factor in a wide variety of plant tissues, and its selectivity in discriminating a single gene family member by the in situ localization of rbcs3 transcripts. Furthermore, we demonstrate the utility of the in-well in situ method in detecting FDL and IFL1 transcripts in Arabidopsis sections, thus establishing the method as a tool to determine spatial **expression pattern** of sequences obtained from genomic sequencing projects. Being amenable to robotic processing, in-well in situ reverse transcription-polymerase chain reaction permits a great enhancement in the number of tissue samples that can be processed. Consequently, this method may become a powerful tool for functional genomics studies, permitting the cellular site of transcription of large numbers of sequences obtained from **databases** to be rapidly **established**.

L25 ANSWER 3 OF 3 MEDLINE
ACCESSION NUMBER: 1999134595 MEDLINE
DOCUMENT NUMBER: 99134595 PubMed ID: 9949436
TITLE: The expression of genes in human preimplantation embryos.
AUTHOR: Pergament E; Fiddler M
CORPORATE SOURCE: Department of Obstetrics and Gynecology, Northwestern University Medical School, Chicago, IL, USA.
SOURCE: PRENATAL DIAGNOSIS, (1998 Dec) 18 (13) 1366-73. Ref: 55
Journal code: 8106540. ISSN: 0197-3851.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903

ENTRY DATE: Entered STN: 19990413
Last Updated on STN: 19990413
Entered Medline: 19990326

AB The study of gene expression in human preimplantation embryos is establishing itself as a necessary dimension of developmental biology and medical genetics. Transcripts identified in human preimplantation embryos include housekeeping genes, transcription and growth factor genes, sex-determining genes, tissue-specific genes and novel genes, as well as genes of unknown function. Strategies are being developed which will eventually permit the most sophisticated gene expression studies on single human embryos of co-ordinated transcription and translational regulation. There is both a need for international co-operation for the systematic construction of expression maps and a need to **establish databases** of **expression patterns** during different stages of human development. Understanding how genes are regulated in humans is essential for understanding both normal development and disease. Until recently, studies of gene expression and regulation during embryogenesis were almost exclusively limited to prokaryotes and to eukaryotes other than man. The introduction of artificial reproductive technologies in conjunction with the development of recombinant molecular technologies applicable to single cells has made possible the study of human development at its earliest stages (Pergament and Bonnicksen, 1994). Although there are still enormous technical challenges, robust strategies have been, and continue to be, developed for connecting DNA sequence to such endophenotypes as timing and level of genes expression at the single cell level. Questions currently being asked in human developmental genetic studies concern the pronucleus, the zygote and the preimplantation embryo: what genes are expressed? When are they expressed? What functions do they perform and how, in sequence or in combination? And, what elements control and regulate their expression? This review provides an overview of current knowledge about the expression of different embryonic genes during early human development and discusses future prospects, which includes a need for international co-operation similar to the Human Genome Project.

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NEWS  3  Jan 29    FSTA has been reloaded and moves to weekly updates
NEWS  4  Feb 01    DKILIT now produced by FIZ Karlsruhe and has a new update
                   frequency
NEWS  5  Feb 19    Access via Tymnet and SprintNet Eliminated Effective 3/31/02
NEWS  6  Mar 08    Gene Names now available in BIOSIS
NEWS  7  Mar 22    TOXLIT no longer available
NEWS  8  Mar 22    TRCTHERMO no longer available
NEWS  9  Mar 28    US Provisional Priorities searched with P in CA/CAplus
                   and USPATFULL
NEWS 10  Mar 28    LIPINSKI/CALC added for property searching in REGISTRY
NEWS 11  Apr 02    PAPERCHEM no longer available on STN.  Use PAPERCHEM2
instead.
NEWS 12  Apr 08    "Ask CAS" for self-help around the clock
NEWS 13  Apr 09    BEILSTEIN: Reload and Implementation of a New Subject Area
NEWS 14  Apr 09    ZDB will be removed from STN
NEWS 15  Apr 19    US Patent Applications available in IFICDB, IFIPAT, and
IFIUDB
NEWS 16  Apr 22    Records from IP.com available in CAPLUS, HCAPLUS, and
ZCAPLUS
NEWS 17  Apr 22    BIOSIS Gene Names now available in TOXCENTER
NEWS 18  Apr 22    Federal Research in Progress (FEDRIP) now available
NEWS 19  Jun 03    New e-mail delivery for search results now available
NEWS 20  Jun 10    MEDLINE Reload
NEWS 21  Jun 10    PCTFULL has been reloaded
NEWS 22  Jul 02    FOREGE no longer contains STANDARDS file segment

NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
              CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
              AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002

=> file medline
COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
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FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002
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 MeSH 2002 vocabulary.  Enter HELP THESAURUS for details.

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L6            21 ORTHOLOG AND PY<1993

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L7           15 ORTHOLOG AND PY<1992

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L7   ANSWER 1 OF 15     MEDLINE
ACCESSION NUMBER:    91342605     MEDLINE
DOCUMENT NUMBER:     91342605   PubMed ID: 1875910
TITLE:               Purification and characterization of the major hepatic
                     cannabinoid hydroxylase in the mouse: a possible member of
                     the cytochrome P-450IIC subfamily.
AUTHOR:              Bornheim L M; Correia M A
CORPORATE SOURCE:    Department of Pharmacology, University of California, San
                     Francisco 94143.
CONTRACT NUMBER:     DA-04265 (NIDA)
                     DK-26506 (NIDDK)
                     DK-26743 (NIDDK)
                     +
SOURCE:              MOLECULAR PHARMACOLOGY, (1991 Aug) 40 (2) 228-34.
                     Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY:        United States
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         199109
ENTRY DATE:          Entered STN: 19911013
                     Last Updated on STN: 19911013
                     Entered Medline: 19910924
AB   Acute cannabidiol treatment of mice inactivated hepatic microsomal
     cytochrome P-450IIIA (P-450IIIA) and markedly inhibited in vitro
     cannabinoid metabolism. Antibodies raised against purified P-450IIIA
     inhibited the microsomal formation of quantitatively minor cannabinoid
     metabolites but had no effect on the major metabolites. Cannabinoid
     hydroxylation to the major metabolites was used as a functional probe to
     isolate and purify a P-450 (termed P-450THC) from hepatic microsomes of
     untreated mice. The purified protein had an apparent molecular weight of
     47,000 and a specific content of 15.4 nmol/mg and exhibited an absorbance
     maximum at 452 nm for the reduced carbon monoxide complex. NH2-terminal
     sequence analysis of the first 16 residues of P-450THC suggests that it
is
     a member of the P-450IIC subfamily, because its sequence is 85 and 69%
     identical to published sequences of rat hepatic P-450IIC7 and P-450IIC6,
     respectively. P-450THC exhibited high activity for cannabinoid
     hydroxylation and specifically produced 6 alpha- and 7-hydroxy-delta
     1-tetrahydrocannabinol, as well as 6 alpha-, 7-, and 4"-
     hydroxycannabidiol. Unlike anti-P-450IIIA antibody, antibody raised
     against purified P-450THC markedly inhibited the microsomal formation of
     all major cannabinoid metabolites. Similar immunoinhibition studies also
     revealed the existence of orthologs of mouse P-450THC and
     P-450IIIA in human liver microsomes. Thus, cannabidiol treatment of mice
     resulted in the inactivation of at least two constitutive P-450 isozymes,
     which together account for the majority of the detected cannabinoid
     metabolites.

L7   ANSWER 2 OF 15     MEDLINE
ACCESSION NUMBER:    91286259     MEDLINE
DOCUMENT NUMBER:     91286259   PubMed ID: 1712018
TITLE:               Cloning, primary sequence, and chromosomal mapping of a
                     human flavin-containing monooxygenase (FMO1).
```

AUTHOR: Dolphin C; Shephard E A; Povey S; Palmer C N; Ziegler D M; Ayesh R; Smith R L; Phillips I R
CORPORATE SOURCE: Department of Biochemistry, Queen Mary and Westfield College, University of London, United Kingdom.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, **(1991 Jul 5)** 266 (19) 12379-85.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M62981; GENBANK-M63116; GENBANK-M63255; GENBANK-M63926; GENBANK-M63977; GENBANK-M63978; GENBANK-M64082; GENBANK-M80558; GENBANK-M80559; GENBANK-M80560
ENTRY MONTH: 199108
ENTRY DATE: Entered STN: 19910825
Last Updated on STN: 19960129
Entered Medline: 19910807

AB cDNA clones that code for a pig and human flavin-containing monooxygenase (FMO) have been isolated. The full-length sequence of the human cDNAs revealed that they encode a polypeptide of 532 amino acid residues containing putative FAD- and NADP-binding sites. The deduced amino acid sequence has 88 and 86% identity, respectively, with the pig and rabbit "hepatic" forms of FMO, but is only 58% similar to the rabbit "pulmonary" FMO, and thus represents the human **ortholog** of the "hepatic" form of FMO. However, as this FMO is present in low abundance in human adult liver, the general term "hepatic" for this form of the enzyme is misleading, and thus we propose the name FMO1 to describe this human FMO and its mammalian **orthologs**. Northern blot analysis demonstrated that human FMO1 mRNA is more abundant in fetal than in adult liver, indicating that in man the enzyme is subject to developmental regulation. Southern blot hybridization of human genomic DNA suggests that the protein is encoded by a single gene, which has been designated FMO1 and mapped to chromosome 1.

L7 ANSWER 3 OF 15 MEDLINE
ACCESSION NUMBER: 91160400 MEDLINE
DOCUMENT NUMBER: 91160400 PubMed ID: 1981509
TITLE: Three N-aralkylated derivatives of 1-aminobenzotriazole as potent and isozyme-selective, mechanism-based inhibitors of guinea pig pulmonary cytochrome P-450 in vitro.
AUTHOR: Woodcroft K J; Szczepan E W; Knickle L C; Bend J R
CORPORATE SOURCE: Department of Pharmacology and Toxicology, University of Western Ontario, London, Canada.
SOURCE: DRUG METABOLISM AND DISPOSITION, **(1990 Nov-Dec)** 18 (6) 1031-7.
Journal code: 9421550. ISSN: 0090-9556.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199104
ENTRY DATE: Entered STN: 19910505
Last Updated on STN: 19950206
Entered Medline: 19910415

AB The potency and cytochrome P-450 (P-450) isozyme selectivity of 1-aminobenzotriazole (ABT) and three of its N-aralkylated analogues, N-benzyl-1-aminobenzotriazole (BBT), N-alpha-methylbenzyl-1-

aminobenzotriazole (alpha MB), and the newly synthesized N-alpha-ethylbenzyl-1-aminobenzotriazole (alpha EB), as mechanism-based inhibitors were compared in pulmonary microsomes of untreated and beta-naphthoflavone (beta-NF)-induced guinea pigs. All four compounds were suicide substrates for pulmonary P-450, resulting in the loss of spectrally assayed hemoprotein (up to 50%). Monooxygenase activities were measured with isozyme-selective/specific substrates; the O-dealkylation of 7-pentoxyresorufin (PRF) for the guinea pig **ortholog** of rabbit P-450IIB4, the O-deethylation of 7-ethoxyresorufin for P-450IA1, and the N-hydroxylation of the aromatic amine 4-aminobiphenyl for P-450IVB1, BBT, alpha MB, and alpha EB were selective for the suicidal inhibition of P-450IIB4; for example, 1 microM alpha MB inactivated 95% of P-450IIB4-, and approximately 10% of P-450IA1- and IVB1-catalyzed, activity in microsomes from beta-NF-induced lungs. Isozyme selectivity was approximately the same for alpha EB and slightly lower for BBT, which inactivated relatively more P-450IA1. At low concentrations, 1 and 10 microM, respectively, ABT preferentially inactivated P-450IVB1, consistent with the efficient N-hydroxylation of aromatic amines by this form of P-450. alpha EB also was shown to efficiently inactivate P-450IIB4-catalyzed PRF activity in microsomes prepared from liver of phenobarbital-induced guinea pigs.(ABSTRACT TRUNCATED AT 250 WORDS)

L7 ANSWER 4 OF 15 MEDLINE

ACCESSION NUMBER: 91113948 MEDLINE
DOCUMENT NUMBER: 91113948 PubMed ID: 2276091
TITLE: N-aralkylated derivatives of 1-aminobenzotriazole as isozyme-selective, mechanism-based inhibitors of guinea pig hepatic cytochrome P-450 dependent monooxygenase activity.
AUTHOR: Woodcroft K J; Bend J R
CORPORATE SOURCE: Department of Pharmacology and Toxicology, University of Western Ontario, London, Canada.
SOURCE: CANADIAN JOURNAL OF PHYSIOLOGY AND PHARMACOLOGY, **(1990 Sep)** 68 (9) 1278-85.
Journal code: 0372712. ISSN: 0008-4212.
PUB. COUNTRY: Canada
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199103
ENTRY DATE: Entered STN: 19910329
Last Updated on STN: 19970203
Entered Medline: 19910304

AB The mechanism-based inactivation of hepatic cytochrome P-450 by the suicide inhibitor 1-aminobenzotriazole and two of its derivatives, N-benzyl-1-aminobenzotriazole and N-alpha-methylbenzyl-1-aminobenzotriazole, was investigated in microsomes from untreated, phenobarbital-induced, and beta-naphthoflavone-induced guinea pigs. Microsomal 7-ethoxyresorufin O-deethylase, 7-pentoxyresorufin O-dealkylase, and benzphetamine N-demethylase activities, and cytochrome P-450 content were determined following incubation with 1-aminobenzotriazole and its analogues. The loss of hepatic cytochrome P-450 content and monooxygenase activity was dependent on inhibitor concentration and required NADPH. N-Benzyl-1-aminobenzotriazole and N-alpha-methylbenzyl-1-aminobenzotriazole were more potent inhibitors of monooxygenase activity than the parent compound in microsomes from untreated and phenobarbital-induced guinea pigs. In microsomes from

phenobarbital-induced guinea pigs, N-alpha-methylbenzyl-1-aminobenzotriazole (10 microM) was highly selective for the inactivation of the major cytochrome P-450 isozyme catalyzing 7-pentoxyresorufin O-dealkylation (the guinea pig **ortholog** of P-450IIB1) compared with those isozymes catalyzing 7-ethoxyresorufin O-deethylation or benzphetamine N-demethylation (88 +/- 3% loss of activity vs. 35 +/- 11 and 13 +/- 7%, respectively). N-Benzyl-1-aminobenzotriazole was also selective for the inactivation of 7-pentoxyresorufin O-dealkylase activity, but to a lesser degree (56 +/- 6 vs. 31 +/- 8 and 21 +/- 8%, respectively). In hepatic microsomes from untreated guinea pigs, the two N-substituted analogues were selective for the inhibition of 7-pentoxyresorufin O-dealkylation compared with benzphetamine N-demethylation, but not 7-ethoxyresorufin O-deethylation.(ABSTRACT TRUNCATED AT 250 WORDS)

L7 ANSWER 5 OF 15 MEDLINE
ACCESSION NUMBER: 91099372 MEDLINE
DOCUMENT NUMBER: 91099372 PubMed ID: 2269307
TITLE: Expression of human liver cytochrome P450 IIIA4 in yeast. A
functional model for the hepatic enzyme.
AUTHOR: Renaud J P; Cullin C; Pompon D; Beaune P; Mansuy D
CORPORATE SOURCE: Centre National de la Recherche Scientifique, Unite de Recherche Associee 400, Paris, France.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, **(1990 Dec 27)** 194 (3) 889-96.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199102
ENTRY DATE: Entered STN: 19910329
Last Updated on STN: 19910329
Entered Medline: 19910220

AB Cytochrome P-450 (P450) NF, a member of the P450 IIIA subfamily, is the major contributor to the oxidation of the calcium-channel blocker nifedipine in human liver microsomes. A cDNA clone designated NF25 encoding for human P450 NF was isolated from a bacteriophage lambda gt11 expression library [Beaune, P. H., Umbenhauer, D. R., Bork, R. W., Lloyd, R. S. & Guengerich, F. P. (1986) Proc. Natl Acad. Sci. USA 83, 8064-8068].

We have expressed NF25 cDNA in Saccharomyces cerevisiae using an expression vector constructed from pYeDP1/8-2 [Cullin, C. & Pompon, D. (1988) Gene 65, 203-217]. Yeast transformed with the plasmid containing the NF25 sequence (pVNF25) showed a ferrous-CO spectrum typical of cytochrome P-450. Microsomal preparations contained a protein with an apparent molecular mass identical to that of P450-5 (a form isolated from human liver indistinguishable from P450 NF) that was not present in microsomes from control yeast (transformed with pYeDP1/8-2 alone), as revealed by immunoblotting with anti-P450-5 antibodies. On the other hand, antibodies raised in rabbits against human liver P450 IIC8-10 and rat liver P450 IA1 and P450 IIE1 did not recognize yeast-expressed P450 NF25. The P450 NF25 content in microsomes was about 90 pmol/mg protein. Microsomal, yeast-expressed P450 NF25 exhibited a high affinity for different substrates including macrolide antibiotics, dihydroergotamine and miconazole as shown by difference visible spectroscopy. Microsomal suspensions containing P450 NF25 were also able to catalyze several oxidation reactions that were expected from the activities of the protein isolated from human liver, including nifedipine 1,4-oxidation, quinidine

3-hydroxylation and N-oxygenation, and N-demethylation of the macrolide antibiotics erythromycin and troleandomycin. The yeast endogenous NADPH-cytochrome P-450 reductase thus couples efficiently with the heterologous P450 NF25 though its level is far lower than that of its **ortholog** in human liver. Indeed addition of rabbit liver NADPH-cytochrome P-450 reductase increased the oxidation rates. Rabbit liver cytochrome b5 also caused a marked enhancement of catalytic activities, as had been noted previously for this particular P450 enzyme in a reconstituted system involving the protein purified from human liver.

Furthermore, the level of the yeast endogenous cytochrome P-450 (lanosterol 14-demethylase) has been found to be negligible compared to the heterologously expressed cytochrome P-450 (30 times less). Thus, yeast microsomes containing P450 NF25 constitute by themselves a good functional model for studying the binding capacities and catalytic activities of this individual form of human hepatic cytochrome P-450.

L7 ANSWER 6 OF 15 MEDLINE

ACCESSION NUMBER: 91087184 MEDLINE
DOCUMENT NUMBER: 91087184 PubMed ID: 2262908
TITLE: Lidocaine metabolism by human cytochrome P-450s purified from hepatic microsomes: comparison of those with rat hepatic cytochrome P-450s.
AUTHOR: Imaoka S; Enomoto K; Oda Y; Asada A; Fujimori M; Shimada T;
Fujita S; Guengerich F P; Funae Y
CORPORATE SOURCE: Laboratory of Chemistry, Osaka City University Medical School, Japan.
SOURCE: JOURNAL OF PHARMACOLOGY AND EXPERIMENTAL THERAPEUTICS, **(1990 Dec)** 255 (3) 1385-91.
Journal code: 0376362. ISSN: 0022-3565.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199102
ENTRY DATE: Entered STN: 19910322
Last Updated on STN: 19910322
Entered Medline: 19910207

AB The metabolism of lidocaine by human hepatic microsomes and purified human cytochrome P-450s, P-450NF (P450IIIA4), P-450MP (a P450IIC form) and P-450PA (P450IA2) was examined and their metabolism was compared with that by rat hepatic cytochrome P-450s. Human hepatic microsomes produced monoethylglycinexylidide (MEGX) and 3-hydroxylidocaine (3-OH-LID) from lidocaine. In a reconstituted system with dilauroylphosphatidylcholine, P-450NF efficiently produced MEGX. P-450PA was not efficient in lidocaine N-deethylation (formation of MEGX) but produced 3-OH-LID. P-450NF and P-450MP did not produce 3-OH-LID. Lidocaine N-deethylation activity of P-450NF was enhanced in a modified reconstituted system with a phospholipid mixture and sodium cholate. P-450NF appears to be an **ortholog** to rat P450 PB-1 (P450IIIA2). Anti-P450 PB-1 antibody cross-reacted with P-450NF and efficiently inhibited lidocaine N-deethylation in human hepatic microsomes. The correlation of lidocaine N-deethylation activity with the concentration of P-450NF determined immunochemically with anti-P450 PB-1 antibody was good (r = 0.81). In addition, correlation between P-450NF content estimated with anti-P450

PB-1 and anti-P-450NF preparations was good (r = 0.96). These results suggest that rat P450 PB-1 and human P-450NF have closely related properties and P-450NF is the major enzyme involved in lidocaine N-deethylation in human hepatic microsomes.

L7 ANSWER 7 OF 15 MEDLINE
ACCESSION NUMBER: 90384440 MEDLINE
DOCUMENT NUMBER: 90384440 PubMed ID: 1698250
TITLE: Interferon down regulates the male-specific cytochrome P450IIIA2 in rat liver.
AUTHOR: Craig P I; Mehta I; Murray M; McDonald D; Astrom A; van der Meide P H; Farrell G C
CORPORATE SOURCE: Department of Medicine, University of Sydney, Westmead Hospital, New South Wales, Australia.
SOURCE: MOLECULAR PHARMACOLOGY, **(1990 Sep)** 38 (3) 313-8. Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199010
ENTRY DATE: Entered STN: 19901122
Last Updated on STN: 19960129
Entered Medline: 19901022

AB The aim of this study was to clarify the mechanism by which cytochrome P450 (P450)-mediated catalytic activity is decreased following interferon (IFN) administration. Microsomal steroid hydroxylation was assessed to test the hypothesis that IFN selectively decreases the activities of individual P450 isozymes in male rats. Thus, recombinant rat IFN gamma (r-rat IFN gamma) treatment produced 40% and 17% reductions in androst-4-ene-3,17-dione (androstenedione) 6 beta- and 16 beta-hydroxylation, respectively. Androstenedione 16 alpha- and 7 alpha-hydroxylation were unaltered following r-rat IFN gamma treatment. Similar changes in the androstenedione hydroxylation pathways were observed following administration of naturally derived rat IFN alpha/beta.
Microsomal levels of P450IIIA2, the male-specific constitutive steroid 6 beta-hydroxylase, were lower after administration of r-rat IFN gamma (42% of control fractions). Furthermore, hepatic P450IIIA2 mRNA was found to be decreased to a similar extent by r-rat IFN gamma. These findings suggest that IFN selectively decreases the content of this isozyme by a mechanism involving altered mRNA regulation. Sex steroids were unlikely to have mediated the decrease in P450IIIA2 levels since serum estradiol and testosterone levels were unchanged by r-rat IFN gamma. In order to determine whether IFN alters the expression of P450IIIA1, a steroid-inducible member of the P450IIIA gene subfamily which is not expressed in untreated rat liver, adult female rats (which lack P450IIIA2) were coadministered pregnenolone 16 alpha-carbonitrile and r-rat IFN gamma. However, IFN failed to impair the induction of androstenedione 6 beta-hydroxylation produced by pregnenolone 16 alpha-carbonitrile. These findings suggest that although IFN decreases the expression of P450IIIA2, it may not down regulate the expression of other steroid-inducible P450IIIA proteins. In view of the existence of human P450IIIA **orthologs** which catalyze the metabolism of several important therapeutic agents, the findings of this study may help predict possible drug interactions in patients receiving IFN.

L7 ANSWER 8 OF 15 MEDLINE

ACCESSION NUMBER: 90169456 MEDLINE
DOCUMENT NUMBER: 90169456 PubMed ID: 2307352
TITLE: The pattern of mammalian evolution and the relative rate of molecular evolution.
AUTHOR: Easteal S
CORPORATE SOURCE: Human Genetics Group, John Curtin School of Medical Research, Australian National University, Canberra ACT.
SOURCE: GENETICS, **(1990 Jan)** 124 (1) 165-73.
Journal code: 0374636. ISSN: 0016-6731.
Report No.: NASA-90169456.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199004
ENTRY DATE: Entered STN: 19900601
Last Updated on STN: 19970203
Entered Medline: 19900404

AB The rates of nucleotide substitution at four genes in four orders of eutherian mammals are compared in relative rate tests using marsupial **orthologs** for reference. There is no evidence of systematic variation in evolutionary rate among the orders. The sequences are used to reconstruct the phylogeny of the orders using maximum likelihood, parsimony and compatibility methods. A branching order of rodent then ungulate then primate and lagomorph is overwhelmingly indicated. The nodes of the nucleotide based cladograms are widely separated in relation to the total lengths of the branches. The assumption of a star phylogeny that underlies Kimura's test for molecular evolutionary rate variation is shown to be invalid for eutherian mammals. Excess variance in nucleotide or amino acid differences between mammalian orders, above that predicted by neutral theory is explained better by variation in divergence time than by variation in evolutionary rate.

L7 ANSWER 9 OF 15 MEDLINE
ACCESSION NUMBER: 90147799 MEDLINE
DOCUMENT NUMBER: 90147799 PubMed ID: 2405858
TITLE: Phenytoin 4-hydroxylation by rabbit liver P450IIC3 and identification of **orthologs** in human liver microsomes.
AUTHOR: Doecke C J; Sansom L N; McManus M E
CORPORATE SOURCE: School of Pharmacy, South Australian Institute of Technology, Adelaide.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, **(1990 Jan 30)** 166 (2) 860-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199003
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19900328
Entered Medline: 19900305

AB The ability of rabbit liver microsomes to 4-hydroxylate phenytoin to 5-(4-hydroxyphenyl)-5-phenylhydantoin was studied. No significant

difference was observed between the capacity of control and rifampicin, phenobarbital, acetone, 2,3,7,8-tetrachlorodibenzo-p-dioxin and phenytoin induced rabbit liver microsomes to 4-hydroxylate phenytoin. In reconstitution experiments using six purified rabbit cytochromes P450 isozymes, only P450IIC3 was capable of 4-hydroxylating phenytoin whereas P450IA1, P450IA2, P450IIB4, P450IIIA6, and P450IVB1 were inactive. Further, anti-P450IIC3 IgG completely inhibited phenytoin 4-hydroxylase activity in rabbit liver microsomes. The above data suggest a major role for the constitutive isozyme P450IIC3 in phenytoin 4-hydroxylase activity in rabbit liver. In human liver microsomes P450IIC3 IgG inhibited phenytoin 4-hydroxylase activity by 66%, suggesting that an **ortholog** to rabbit P450IIC3 is in part responsible for this activity in man.

L7 ANSWER 10 OF 15 MEDLINE
ACCESSION NUMBER: 90106866 MEDLINE
DOCUMENT NUMBER: 90106866 PubMed ID: 2403855
TITLE: Metabolic deactivation of furylfuramide by cytochrome P450 in human and rat liver microsomes.
AUTHOR: Shimada T; Yamazaki H; Shimura H; Tanaka R; Guengerich F P
CORPORATE SOURCE: Osaka Prefectural Institute of Public Health, Japan.
SOURCE: CARCINOGENESIS, **(1990 Jan)** 11 (1) 103-10.
Journal code: 8008055. ISSN: 0143-3334.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199002
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19970203
Entered Medline: 19900222

AB Metabolic deactivation of furylfuramide by human and rat liver microsomal cytochrome P450 enzymes has been investigated in a system measuring induction of umu gene expression response in Salmonella typhimurium TA1535/pSK1002. Both human and rat liver microsomes catalyzed the metabolism of furylfuramide to inactive form(s) that are incapable of inducing umu gene expression in the tester strain. The reaction required an NADPH-generating system and molecular oxygen and was inhibited by carbon monoxide, suggesting that a cytochrome P450-linked mono-oxygenase system is prerequisite for the deactivation reaction. With liver microsomes from variously pretreated rats, 3-methylcholanthrene was found to be a powerful inducer for the furylfuramide-metabolizing activity, and antibodies raised against rat P450IA1(BNF-B, c) and P450IA2(ISF-G, d) inhibited the microsomal activity. Human liver microsomal furylfuramide-metabolizing activity was also inhibited significantly by anti-P450IA2 IgG but weakly by anti-P450IA1 IgG. In liver microsomes prepared from seven different human samples, the activities of deactivation of furylfuramide were found to correlate with the amounts of immunoreactive protein related to rat P450IA2 and with the monooxygenase activities of metabolic activation of 2-amino-3,4-dimethyl-imidazo[4,5-f]quinoline (MeIQ) and of ethoxyresorufin O-deethylation. These results suggest that P450IA1 and P450IA2 in rats, and P450PA (IA2, the phenacetin O-deethylase and **ortholog** of rat P450IA2) in humans are the major enzymes involved in the deactivation of furylfuramide in liver microsomes. The metabolic studies involving HPLC analysis of products followed by spectrophotometric examination have also suggested that furylfuramide can be degraded very rapidly through the aerobic metabolism by liver microsomes.

L7 ANSWER 11 OF 15 MEDLINE
ACCESSION NUMBER: 90046662 MEDLINE

DOCUMENT NUMBER: 90046662 PubMed ID: 2813353
TITLE: Human cytochrome P-450PA (P-450IA2), the phenacetin O-deethylase, is primarily responsible for the hepatic 3-demethylation of caffeine and N-oxidation of carcinogenic arylamines.
AUTHOR: Butler M A; Iwasaki M; Guengerich F P; Kadlubar F F
CORPORATE SOURCE: Division of Biochemical Toxicology, National Center for Toxicological Research, Jefferson, AR 72079.
CONTRACT NUMBER: CA 44353 (NCI)
ES 00267 (NIEHS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, **(1989 Oct)** 86 (20) 7696-700.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198912
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19970203
Entered Medline: 19891201

AB Aromatic amines are well known as occupational carcinogens and are found in cooked foods, tobacco smoke, synthetic fuels, and agricultural chemicals. For the primary arylamines, metabolic N-oxidation by hepatic cytochromes P-450 is generally regarded as an initial activation step leading to carcinogenesis. The metabolic activation of 4-aminobiphenyl, 2-naphthylamine, and several heterocyclic amines has been shown recently to be catalyzed by rat cytochrome P-450ISF-G and by its human **ortholog**, cytochrome P-450PA. We now report that human hepatic microsomal caffeine 3-demethylation, the initial major step in caffeine biotransformation in humans, is selectively catalyzed by cytochrome P-450PA. Caffeine 3-demethylation was highly correlated with 4-aminobiphenyl N-oxidation ($r = 0.99$; P less than 0.0005) in hepatic microsomal preparations obtained from 22 human organ donors, and both activities were similarly decreased by the selective inhibitor, 7,8-benzoflavone. The rates of microsomal caffeine 3-demethylation, 4-aminobiphenyl N-oxidation, and phenacetin O-deethylation were also significantly correlated with each other and with the levels of immunoreactive human cytochrome P-450PA. Moreover, a rabbit polyclonal antibody raised to human cytochrome P-450PA was shown to inhibit strongly all three of these activities and to inhibit the N-oxidation of the carcinogen 2-naphthylamine and the heterocyclic amines, 2-amino-6-methyldipyrido-[1,2-a:3',2'-d]imidazole and 2-amino-3-methylimidazo[4,5-f]-quinoline. Human liver cytochrome P-450PA was also shown to catalyze caffeine 3-demethylation, 4-aminobiphenyl N-oxidation, and phenacetin O-deethylation. Thus, estimation of caffeine 3-demethylation activity in humans may be useful in the characterization of arylamine N-oxidation phenotypes and in the assessment of whether or not the hepatic levels of cytochrome P-450PA, as affected by environmental or genetic factors, contribute to interindividual differences in susceptibility to arylamine-induced cancers.

L7 ANSWER 12 OF 15 MEDLINE
ACCESSION NUMBER: 90030215 MEDLINE
DOCUMENT NUMBER: 90030215 PubMed ID: 2509067
TITLE: Roles of individual human cytochrome P-450 enzymes in the bioactivation of benzo(a)pyrene, 7,8-dihydroxy-7,8-dihydrobenzo(a)pyrene, and other dihydrodiol derivatives of

polycyclic aromatic hydrocarbons.

AUTHOR: Shimada T; Martin M V; Pruess-Schwartz D; Marnett L J; Guengerich F P

CORPORATE SOURCE: Department of Biochemistry, Vanderbilt University School of Medicine, Nashville, Tennessee 37232.

CONTRACT NUMBER: CA 44353 (NCI)
CA 47479 (NCI)
ES 00267 (NIEHS)

SOURCE: CANCER RESEARCH, **(1989 Nov 15)** 49 (22) 6304-12.
Journal code: 2984705R. ISSN: 0008-5472.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198912

ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19970203
Entered Medline: 19891211

AB Human liver microsomes oxidized 7,8-dihydroxy-7,8-dihydrobenzo(a)pyrene [B(a)P-7,8-diol] to products that yield DNA adduct formation and umu gene expression in the tester system Salmonella typhimurium TA1535/pSK1002. The umu response is correlated to levels of microsomal cytochrome P-450NF (P-450NF) and nifedipine oxidation in different human liver samples used for activation, and both the (+)- and (-)-enantiomers of B(a)P-7,8-diol gave similar results in these and other assays. The microsomal umu response was inhibited by antibodies raised against P-450NF. 7,8-Benzoflavone stimulated the B(a)P-7,8-diol-dependent umu response observed with purified P-450NF and human liver and lung microsomes. Thus, P-450NF appears to be the major enzyme involved in the activation of B(a)P-7,8-diol in human liver and possibly lung. Similar results were obtained for the activation of trans-9,10-dihydroxy-9,10-dihydrobenzo(b)fluoranthene and trans-3,4-dihydroxy-3,4-dihydro-7,12-dimethylbenz(a)anthracene, compounds that are known to form highly tumorigenic diol-epoxides. The major product of the oxidation of (+)-B(a)P-7,8-diol was the cis-syn isomer of benzo(a)pyrene-7,8,9,10-tetraol[7 beta, 8 alpha, 9 beta, 10 beta-tetrahydroxy-7,8,9,10-tetrahydrobenzo(a)pyrene]. Studies on the nature of the human liver enzymes involved in the formation of B(a)P-7,8-diol [from benzo(a)pyrene] indicate that neither P-450NF, P-450PA, P-450j, P-450DB, nor P-450MP is involved. The correlation of 7,8-diol formation with phenacetin O-deethylation in a set of liver samples and the partial inhibition of the reaction by 7,8-benzoflavone and anti-rat P-450 beta NF-B suggest that the enzyme involved may be P1-450, the human **ortholog** of rat P-450 beta NF-B, which catalyzes both the formation of B(a)P-7,8-diol and its subsequent oxidation in tissues of polycyclic hydrocarbon-treated rats. The differential effects of inhibitors indicate that benzo(a)pyrene 3-hydroxylation, 4,5-epoxidation, and 9,10-epoxidation are catalyzed by an enzyme(s) distinct from that which forms the 7,8-epoxide. The roles of the human P-450 enzymes differ from the rodent **orthologs** in the paradigm for bioactivation of polycyclic hydrocarbons; further, flavones appear to have opposing effects on diol formation and further epoxidation in both human liver and lung.

L7 ANSWER 13 OF 15 MEDLINE

ACCESSION NUMBER: 89313716 MEDLINE

DOCUMENT NUMBER: 89313716 PubMed ID: 2747631
TITLE: Induction and tissue-specific expression of rabbit cytochrome P450IIE1 and IIE2 genes.
AUTHOR: Porter T D; Khani S C; Coon M J
CORPORATE SOURCE: Department of Biological Chemistry, Medical School, University of Michigan, Ann Arbor 48109.
CONTRACT NUMBER: AA-06221 (NIAAA)
GM-07863 (NIGMS)
SOURCE: MOLECULAR PHARMACOLOGY, **(1989 Jul)** 36 (1) 61-5.
Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198908
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19980206
Entered Medline: 19890822

AB Treatment of rabbits with a variety of dissimilar chemicals, including ethanol, acetone, and imidazole, results in elevated levels of hepatic and renal cytochrome P-450 form 3a, also designated P-450ALC or P-450IIE. The P450IIE1 subfamily in rabbits is composed of two genes that encode proteins with 97% sequence identity; the mRNAs from these genes can be distinguished by their differing electrophoretic mobilities. In the present studies, examination of the expression of these genes revealed that P450IIE1 (gene 1) mRNA is present in greatest abundance in the liver, is present in kidney and nasal mucosa at approximately 10% of the level in liver, and is present in lung at approximately 5% of the level in liver. P450IIE2 (gene 2) mRNA is present in liver and lung at approximately 50% of the level of gene 1 mRNA in these tissues but cannot be detected in kidney or nasal mucosa. Neither gene is expressed in testis, ovary, small intestine, or adrenal tissue. Treatment of rabbits with acetone or imidazole results in elevated levels of P-450 3a-immunoreactive protein in liver and kidney without concomitant increases in P450IIE gene mRNAs. Moreover, various lengths of ethanol treatment elevated the level of immunoreactive protein in liver and kidney, with a rapid reduction of gene 1 mRNA and, at 14 days, gene 2 mRNA to approximately 50% of control levels. In contrast to these chemical inducers of 3a, fasting for 48 hr significantly increases gene 1 and 2 mRNA in liver but does not increase the level of immunoreactive protein. These results indicate that the rabbit P450IIE genes are not coordinately expressed or regulated and, as found with the rat **ortholog** P-450j, chemical inducers of 3a evidently act through changes in the rate of synthesis or degradation of the enzyme, rather than through increased gene transcription.

L7 ANSWER 14 OF 15 MEDLINE
ACCESSION NUMBER: 88018021 MEDLINE
DOCUMENT NUMBER: 88018021 PubMed ID: 3116671
TITLE: Phylogenetic relations of humans and African apes from DNA sequences in the psi eta-globin region.
AUTHOR: Miyamoto M M; Slightom J L; Goodman M
CORPORATE SOURCE: Department of Anatomy and Cell Biology, Wayne State University School of Medicine, Detroit, MI 48201.
CONTRACT NUMBER: RO1 HL 33940 (NHLBI)
SOURCE: SCIENCE, **(1987 Oct 16)** 238 (4825) 369-73.
Journal code: 0404511. ISSN: 0036-8075.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J00093; GENBANK-J00094; GENBANK-J00096;
GENBANK-J00158; GENBANK-J00159; GENBANK-J00160;
GENBANK-J00161; GENBANK-J00162; GENBANK-J00163;
GENBANK-J00164; GENBANK-J00165; GENBANK-J00166;
GENBANK-J00167; GENBANK-J00168; GENBANK-J00169;
GENBANK-J00170; GENBANK-J00171; GENBANK-J00172;
GENBANK-J00173; GENBANK-J00174; GENBANK-J00175;
GENBANK-J00177; GENBANK-J00178; GENBANK-J00179;
GENBANK-K01239; GENBANK-K01890; GENBANK-K02542;
GENBANK-K02543; GENBANK-K02544; GENBANK-M18037; +
ENTRY MONTH: 198711
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19980206
Entered Medline: 19871116

AB Sequences from the upstream and downstream flanking DNA regions of the psi eta-globin locus in Pan troglodytes (common chimpanzee), Gorilla gorilla (gorilla), and Pongo pygmaeus (orangutan, the closest living relative to Homo, Pan, and Gorilla) provided further data for evaluating the phylogenetic relations of humans and African apes. These newly sequenced **orthologs** [an additional 4.9 kilobase pairs (kbp) for each species] were combined with published psi eta-gene sequences and then compared to the same orthologous stretch (a continuous 7.1-kbp region) available for humans. Phylogenetic analysis of these nucleotide sequences by the parsimony method indicated (i) that human and chimpanzee are more closely related to each other than either is to gorilla and (ii) that the slowdown in the rate of sequence evolution evident in higher primates is especially pronounced in humans. These results indicate that features (for example, knuckle-walking) unique to African apes (but not to humans) are primitive and that even local molecular clocks should be applied with caution.

L7 ANSWER 15 OF 15 MEDLINE
ACCESSION NUMBER: 87208040 MEDLINE
DOCUMENT NUMBER: 87208040 PubMed ID: 3577206
TITLE: Polymorphism of human cytochrome P-450.
AUTHOR: Guengerich F P; Umbenhauer D R; Churchill P F; Beaune P H; Bocker R; Knodell R G; Martin M V; Lloyd R S
CONTRACT NUMBER: CA 30907 (NCI)
ES 00267 (NIEHS)
SOURCE: XENOBIOTICA, **(1987 Mar)** 17 (3) 311-6.
Journal code: 1306665. ISSN: 0049-8254.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198706
ENTRY DATE: Entered STN: 19900303
Last Updated on STN: 19970203
Entered Medline: 19870605

AB The cytochrome P-450 forms involved in debrisoquine 4-hydroxylation (P-450DB), phenacetin O-deethylation (P-450PA), S-mephenytoin 4-hydroxylation (P-450MP), and nifedipine 1,4-oxidation (P-450NF) have been purified to electrophoretic homogeneity from human liver microsomes. All of these reactions show in vivo polymorphism in humans. Evidence for the roles of the purified proteins in these processes comes from in vitro

reconstitution and immunoinhibition studies. The rat **orthologs** of these enzymes are as follows--P-450DB: P-450UT-H; P-450PA: P-450ISF-G; P-450MP: P-450UT-I; P-450NF: P-450PCN-E. Only in the case of P-450UT-H is the primary rat **ortholog** the same cytochrome P-450 which catalyses the catalytic reaction under consideration. Reconstitution and immunochemical studies establish that the following reactions are catalysed by the individual P-450s--P-450DB: debrisoquine 4-hydroxylation, sparteine delta 5-oxidation, bufuralol 1'-hydroxylation, encainide O-demethylation, and propanolol 4-hydroxylation; P-450PA: phenacetin O-deethylation; P-450MP: S-mephenytoin 4-hydroxylation and tolbutamide methyl hydroxylation; P-450NF: oxidation of nifedipine and 16 other substituted dihydropyridines, estradiol 2- and 4-hydroxylation, aldrin epoxidation, benzphetamine N-demethylation and 6 beta-hydroxylation of testosterone, androstenedione and cortisol. A cDNA clone has been isolated that corresponds to rat P-450UT-H, as shown by a number of criteria. Studies with this probe establish that the sex and strain variation in debrisoquine 4-hydroxylase and related activities is related to differences in the levels of a 2.0 kb length mRNA present. (ABSTRACT TRUNCATED AT 250 WORDS)

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L9           0 L8 AND NADRIN#

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L10         26 L8 AND (RAS(W) LIKE)

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L11       1054 KETCHUM?/AU

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L12       1550 (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
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=> s beasley?/au
L13        4464 BEASLEY?/AU

=> s l11 or l12 or l13
L14        6870 L11 OR L12 OR L13

=> s l14 and (nadrin# or (ras(w)like))
L15           0 L14 AND (NADRIN# OR (RAS(W) LIKE))

=> dup rem l10
PROCESSING COMPLETED FOR L10
L16           10 DUP REM L10 (16 DUPLICATES REMOVED)

=> d ibib abs tot

L16  ANSWER 1 OF 10     MEDLINE                              DUPLICATE 1
ACCESSION NUMBER:   2001295584     MEDLINE
DOCUMENT NUMBER:    21272211   PubMed ID: 11378394
TITLE:              A localized GTPase exchange factor, Bud5, determines the
                    orientation of division axes in yeast.
COMMENT:            Comment in: Curr Biol. 2001 Aug 7;11(15):R610-2
AUTHOR:             Marston A L; Chen T; Yang M C; Belhumeur P; Chant
                    J
CORPORATE SOURCE:   Department of Molecular and Cellular Biology, Harvard
                    University, 7 Divinity Avenue, Cambridge, MA 02138, USA.
CONTRACT NUMBER:    GM49782 (NIGMS)
SOURCE:             CURRENT BIOLOGY, (2001 May 15) 11 (10) 803-7.
                    Journal code: 9107782. ISSN: 0960-9822.
PUB. COUNTRY:       England: United Kingdom
                    Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200107
ENTRY DATE:         Entered STN: 20010716
                    Last Updated on STN: 20020424
                    Entered Medline: 20010712
AB   GTPases are widespread in directing cytoskeletal rearrangements and
     affecting cellular organization. How they do so is not well understood.
     Yeast cells divide by budding, which occurs in two spatially programmed
     patterns, axial or bipolar [1-3]. Cytoskeletal polarization to form a bud
     is governed by the Ras-like GTPase, Bud1/Rsr1, in
     response to cortical landmarks. Bud1 is uniformly distributed on the
     plasma membrane, so presumably its regulators, Bud5 GTPase exchange
factor
     and Bud2 GTPase activating protein, impart spatial specificity to Bud1
     action [4]. We examined the localizations of Bud5 and Bud2. Both Bud1
     regulators associate with cortical landmarks designating former division
     sites. In haploids, Bud5 forms double rings that encircle the mother-bud
     neck and split upon cytokinesis so that each progeny cell inherits Bud5
at
     the axial division remnant. Recruitment of Bud5 into these structures
     depends on known axial landmark components. In cells undergoing bipolar
     budding, Bud5 associates with multiple sites, in response to the bipolar
     landmarks. Like Bud5, Bud2 associates with the axial division remnant,
but
     rather than being inherited, Bud2 transiently associates with the remnant
     in late G1, before condensing into a patch at the incipient bud site. The
     relative timing of Bud5 and Bud2 localizations suggests that both
     regulators contribute to the spatially specific control of Bud1 GTPase.
```

L16 ANSWER 2 OF 10 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001010734 MEDLINE
DOCUMENT NUMBER: 20428418 PubMed ID: 10970842
TITLE: A novel Golgi membrane protein is part of a GTPase-binding protein complex involved in vesicle targeting.
AUTHOR: Matern H; **Yang X**; Andrulis E; Sternglanz R; Trepte H H; Gallwitz D
CORPORATE SOURCE: Department of Molecular Genetics, Max Planck Institute for Biophysical Chemistry, 37070 Gottingen, Germany.
CONTRACT NUMBER: GM28220 (NIGMS)
SOURCE: EMBO JOURNAL, (2000 Sep 1) 19 (17) 4485-92.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001024

AB Through two-hybrid interactions, protein affinity and localization studies, we previously identified Yip1p, an integral yeast Golgi membrane protein able to bind the **Ras-like** GTPases Ypt1p and Ypt31p in their GDP-bound conformation. In a further two-hybrid screen, we identified Yif1p as an interacting factor of Yip1p. We show that Yif1p is an evolutionarily conserved, essential 35.5 kDa transmembrane protein that forms a tight complex with Yip1p on Golgi membranes. The hydrophilic N-terminal half of Yif1p faces the cytosol, and according to two-hybrid analyses can interact with the transport GTPases Ypt1p, Ypt31p and Sec4p, but in contrast to Yip1p, this interaction is dispensable for Yif1 protein function. Loss of Yif1p function in conditional-lethal mutants results in a block of endoplasmic reticulum (ER)-to-Golgi protein transport and in an accumulation of ER membranes and 40-50 nm vesicles. Genetic analyses suggest that Yif1p acts downstream of Yip1p. It is inferred that Ypt GTPase binding to the Yip1p-Yif1p complex is essential for and precedes vesicle docking and fusion.

L16 ANSWER 3 OF 10 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1998393537 MEDLINE
DOCUMENT NUMBER: 98393537 PubMed ID: 9724632
TITLE: Specific binding to a novel and essential Golgi membrane protein (Yip1p) functionally links the transport GTPases Ypt1p and Ypt31p.
AUTHOR: **Yang X**; Matern H T; Gallwitz D
CORPORATE SOURCE: Max Planck Institute for Biophysical Chemistry, Department of Molecular Genetics, D-37070 Gottingen, Germany.
SOURCE: EMBO JOURNAL, (1998 Sep 1) 17 (17) 4954-63.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X97342
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981123

AB The regulation of vesicular transport in eukaryotic cells involves **Ras-like** GTPases of the Ypt/Rab family. Studies in yeast and mammalian cells indicate that individual family members act in vesicle docking/fusion to specific target membranes. Using the two-hybrid system, we have now identified a 248 amino acid, integral membrane protein, termed Yip1, that specifically binds to the transport GTPases Ypt1p and Ypt31p. Evidence for physical interaction of these GTPases with Yip1p was also demonstrated by affinity chromatography and/or co-immunoprecipitation. Like the two GTPases, Yip1p is essential for yeast cell viability and, according to subcellular fractionation and indirect immunofluorescence, is located to Golgi membranes at steady state. Mutant cells depleted of Yip1p and conditionally lethal yip1 mutants at the non-permissive temperature massively accumulate endoplasmic reticulum membranes and display aberrations in protein secretion and glycosylation of secreted invertase. The results suggests for a role for Yip1p in recruiting the two GTPases to Golgi target membranes in preparation for fusion.

L16 ANSWER 4 OF 10 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 4

ACCESSION NUMBER: 1995:97228 BIOSIS
DOCUMENT NUMBER: PREV199598111528
TITLE: Study of Rab6, a **Ras-like** GTP-binding protein associated with the golgi complex.
AUTHOR(S): Goud, Bruno; **Yang, Chunzhi**; Roa, Michele; Martinez, Olivier; Slepnev, Vladimir
CORPORATE SOURCE: Unite de Genetique Somatique, Institut Pasteur, 25 rue du Dr. Roux, 75724 Paris Cedex 15 France
SOURCE: Wiedenmann, B. [Editor]; Kvols, L. K. [Editor]; Arnold, R. [Editor]; Riecken, E. O. [Editor]. Annals of the New York Academy of Sciences, (1994) Vol. 733, pp. 340-343. Annals of the New York Academy of Sciences; Molecular and cell biological aspects of gastroenteropancreatic neuroendocrine tumor disease.
Publisher: New York Academy of Sciences 2 East 63rd Street, New York, New York 10021, USA.
Meeting Info.: Conference Berlin, Germany November 3-7, 1993
ISSN: 0077-8923. ISBN: 0-89766-898-7 (paper), 0-89766-897-9 (cloth).
DOCUMENT TYPE: Book; Conference
LANGUAGE: English

L16 ANSWER 5 OF 10 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 95069591 MEDLINE
DOCUMENT NUMBER: 95069591 PubMed ID: 7978884
TITLE: Study of rab6, a **ras-like** GTP-binding protein associated with the Golgi complex.
AUTHOR: Goud B; **Yang C**; Roa M; Martinez O; Slepnev V
SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1994 Sep 15) 733 340-3. Ref: 29
Journal code: 7506858. ISSN: 0077-8923.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199412
ENTRY DATE: Entered STN: 19950110
Last Updated on STN: 20000303
Entered Medline: 19941202

L16 ANSWER 6 OF 10 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 94205879 MEDLINE
DOCUMENT NUMBER: 94205879 PubMed ID: 8154747
TITLE: Study of rab6, a **ras-like** GTP-binding protein associated with the Golgi complex.
AUTHOR: Goud B; **Yang C**; Roa M; Martinez O; Mayau V
CORPORATE SOURCE: Unite de Genetique Somatique, Institut Pasteur, Paris, France.
SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1994 Mar 9) 710 192-5. Ref: 29
Journal code: 7506858. ISSN: 0077-8923.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199405
ENTRY DATE: Entered STN: 19940523
Last Updated on STN: 20000303
Entered Medline: 19940509

L16 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:123573 CAPLUS
DOCUMENT NUMBER: 122:99578
TITLE: Study of rab6, a **ras-like** GTP-binding protein associated with the Golgi complex
AUTHOR(S): Goud, B.; **Yang, C.**; Roa, M.; Martinez, O.; Mayau, V.
CORPORATE SOURCE: Unite de Genetique Somatique, Institut Pasteur, Paris,
75724, Fr.
SOURCE: Challenges Mod. Med. (1994), 6(GTPase-Controlled Molecular Machines), 181-6
CODEN: CHMME3
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review and discussion with 30 refs. Intracellular localization of RAB6,
function of RAB6, and biochem. of RAB6 were discussed.

L16 ANSWER 8 OF 10 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1994:102718 BIOSIS
DOCUMENT NUMBER: PREV199497115718
TITLE: Study of rab6p, a **ras-like** small GTP-binding protein associated with the Golgi complex.
AUTHOR(S): Goud, B.; Roa, M.; Martinez, O.; **Yang, C.**; Slepnev, V.
CORPORATE SOURCE: Unite Genetique Somatique, Inst. Pasteur, 25 Rue du Dr Roux, 75724 Paris Cedex 15 France
SOURCE: Toxicon, (1993) Vol. 31, No. 12, pp. 1495.
Meeting Info.: International Conference on Toxins and

Exocytosis Gozd Martuljek, Slovenia May 23-28, 1993
ISSN: 0041-0101.
DOCUMENT TYPE: Conference
LANGUAGE: English

L16 ANSWER 9 OF 10 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 94039123 MEDLINE
DOCUMENT NUMBER: 94039123 PubMed ID: 8223626
TITLE: Comparison of the biochemical properties of unprocessed and
processed forms of the small GTP-binding protein, rab6p.
AUTHOR: **Yang C**; Mollat P; Chaffotte A; McCaffrey M; Cabanie L; Goud B
CORPORATE SOURCE: Unite de Genetique Somatique, URA CNRS 361, Institut Pasteur, Paris, France.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1993 Nov 1) 217 (3) 1027-37.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199312
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 20000303
Entered Medline: 19931222

AB The rab6 protein (rab6p) belongs to a large family of **ras-like** low-molecular-mass GTP-binding proteins thought to be involved in the regulation of intracellular transport in mammalian cells. When expressed in the baculovirus/insect cell system, two major forms of rab6p are obtained; a 24-kDa cytosolic unprocessed form and a 23-kDa membrane-bound form which represents the processed lipid-modified protein.

Here, we have purified both forms to homogeneity and we have studied and compared their biochemical properties. Unprocessed and processed rab6p display similar binding-rate constants (kon) for GDP and GTP (1-1.9 microM-1 min-1). However, significant differences exist in the dissociation constants of bound guanine nucleotides. Processed rab6p in low and high magnesium solutions displays similar koff values for GTP and GDP. However, unprocessed rab6p has a koff value higher for GDP than for GTP in both low and high magnesium solutions. Their intrinsic GTPase activities also differ; unprocessed rab6p has an almost undetectable GTPase activity, whereas that of processed rab6p is in the same range as that reported for other ras and **ras-like** GTP-binding proteins (0.012 +/- 0.002 min-1). These results suggest that post-translational modifications of rab6p might induce subtle changes in the three-dimensional structure of the protein which affect the guanine-nucleotide-binding/hydrolysis activity.

L16 ANSWER 10 OF 10 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 92171973 MEDLINE
DOCUMENT NUMBER: 92171973 PubMed ID: 1540193
TITLE: Characterization of the unprocessed and processed forms of rab6 expressed in baculovirus/insect cell systems.
AUTHOR: **Yang C**; Mayau V; Godeau F; Goud B
CORPORATE SOURCE: Unite de Genetique Somatique, URA CNRS 361, INSERM U 277, Institut Pasteur, Paris, France.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1992 Feb 14) 182 (3) 1499-505.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199203
ENTRY DATE: Entered STN: 19920417
Last Updated on STN: 20000303
Entered Medline: 19920327

AB Rab6 protein (rab6p) belongs to a family of **ras-like** GTP-binding proteins thought to be involved in the regulation of intracellular transport in mammalian cells. We have constructed a recombinant baculovirus in order to express rab6p in insect cells. We report here the characterization of four forms of this protein which are found in cytosolic and membrane fractions of infected Sf9 cells. The two major forms are a cytosolic 24 kD protein which represents the unprocessed precursor form of rab6p and a membrane-bound isoprenylated 23 kD protein which represents the processed form. Two other minor forms were also detected: a cytosolic isoprenylated 23 kD protein which may represent a pool in equilibrium with the 23 kD membrane-bound form and a 24 kD non-isoprenylated membrane-bound form which may represent an intermediate in the processing of rab6p.

=> log h

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	28.86	42.33

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-0.62	-0.62

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 15:22:48 ON 09 JUL 2002

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SESSION RESUMED IN FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS'
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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	28.86	42.33

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)        SINCE FILE      TOTAL
                                                       ENTRY    SESSION
CA SUBSCRIBER PRICE                                    -0.62      -0.62

=> d history

     (FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002)

     FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002
L1           168 S ORTHOLOG AND PY<1998
L2           106 S ORTHOLOG AND PY<1997
L3            65 S ORTHOLOG AND PY<1996
L4            42 S ORTHOLOG AND PY<1995
L5            27 S ORTHOLOG AND PY<1994
L6            21 S ORTHOLOG AND PY<1993
L7            15 S ORTHOLOG AND PY<1992

     FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT
     15:19:03 ON 09 JUL 2002
L8        350284 S YAN?/AU
L9             0 S L8 AND NADRIN#
L10           26 S L8 AND (RAS(W)LIKE)
L11         1054 S KETCHUM?/AU
L12         1550 S (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13         4464 S BEASLEY?/AU
L14         6870 S L11 OR L12 OR L13
L15            0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
L16           10 DUP REM L10 (16 DUPLICATES REMOVED)

=> s l8 and (virtual)
L17          164 L8 AND (VIRTUAL)

=> s l8 and (virtual(3a)northern)
L18            0 L8 AND (VIRTUAL(3A) NORTHERN)

=> s l14 and (virtual(3a)northern)
L19            0 L14 AND (VIRTUAL(3A) NORTHERN)

=> d history

     (FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002)

     FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002
L1           168 S ORTHOLOG AND PY<1998
L2           106 S ORTHOLOG AND PY<1997
L3            65 S ORTHOLOG AND PY<1996
L4            42 S ORTHOLOG AND PY<1995
L5            27 S ORTHOLOG AND PY<1994
L6            21 S ORTHOLOG AND PY<1993
L7            15 S ORTHOLOG AND PY<1992

     FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT
     15:19:03 ON 09 JUL 2002
L8        350284 S YAN?/AU
L9             0 S L8 AND NADRIN#
L10           26 S L8 AND (RAS(W)LIKE)
L11         1054 S KETCHUM?/AU
L12         1550 S (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13         4464 S BEASLEY?/AU
L14         6870 S L11 OR L12 OR L13
L15            0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
```

```
L16           10 DUP REM L10 (16 DUPLICATES REMOVED)
L17          164 S L8 AND (VIRTUAL)
L18            0 S L8 AND (VIRTUAL(3A)NORTHERN)
L19            0 S L14 AND (VIRTUAL(3A)NORTHERN)

=> log h
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                        38.68      52.15

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)              SINCE FILE      TOTAL
                                                           ENTRY    SESSION
CA SUBSCRIBER PRICE                                        -0.62      -0.62

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SESSION RESUMED IN FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS,
CAPLUS'
AT 15:27:07 ON 09 JUL 2002
FILE 'MEDLINE' ENTERED AT 15:27:07 ON 09 JUL 2002
FILE 'BIOSIS' ENTERED AT 15:27:07 ON 09 JUL 2002
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COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                        38.68      52.15

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)              SINCE FILE      TOTAL
                                                           ENTRY    SESSION
CA SUBSCRIBER PRICE                                        -0.62      -0.62

<------User Break------>
u
SEARCH ENDED BY USER
SEARCH ENDED BY USER

=> s (mRNA or cDNA or polynucleotide# or transcript#)(3a)express?
   4 FILES SEARCHED...
L20     266508 (MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#)(3A) EXPRESS?

=> s (protein# or peptide# or translat?)(3a)express?
   2 FILES SEARCHED...
   3 FILES SEARCHED...
L21     336550 (PROTEIN# OR PEPTIDE# OR TRANSLAT?)(3A) EXPRESS?
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=> s l20(s)l21
L22      37711 L20(S) L21

=> s Est or ests or (expressed(3w)tag#)
L23     183803 EST OR ESTS OR (EXPRESSED(3W) TAG#)

=> s l22(s)l23
L24        286 L22(S) L23

=> s l24(s)database#
L25        100 L24(S) DATABASE#

=> dup rem l25
PROCESSING COMPLETED FOR L25
L26         35 DUP REM L25 (65 DUPLICATES REMOVED)

=> d ibib abs tot

L26  ANSWER 1 OF 35     MEDLINE                          DUPLICATE 1
ACCESSION NUMBER:   2002185034     MEDLINE
DOCUMENT NUMBER:    21917691   PubMed ID: 11920606
TITLE:              Identification of cancer/testis genes by database mining
                    and mRNA expression analysis.
AUTHOR:             Scanlan Matthew J; Gordon Claudia M; Williamson Barbara;
                    Lee Sang-Yull; Chen Yao-Tseng; Stockert Elisabeth;
                    Jungbluth Achim; Ritter Gerd; Jager Dirk; Jager Elke;
Knuth
                    Alexander; Old Lloyd J
CORPORATE SOURCE:   Ludwig Institute for Cancer Research, New York Branch at
                    Memorial Sloan-Kettering Cancer Center, New York, NY
10021,
                    USA.. scanlanm@mskcc.org
SOURCE:             INTERNATIONAL JOURNAL OF CANCER, (2002 Apr 1) 98 (4)
                    485-92.
                    Journal code: 0042124. ISSN: 0020-7136.
PUB. COUNTRY:       United States
                    Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200205
ENTRY DATE:         Entered STN: 20020403
                    Last Updated on STN: 20020511
                    Entered Medline: 20020510
AB   Cancer/testis (CT) antigens are immunogenic proteins
     expressed predominantly in gametogenic tissue and cancer; they are
     considered promising target molecules for cancer vaccines. The
     identification of new CT genes is essential to the development of
     polyvalent cancer vaccines designed to overcome tumor heterogeneity and
     antigen loss. In the current study, a search for new CT genes was
     conducted by mining the Unigene database for gene clusters that
     contain expressed sequence tags derived solely from
     both normal testis and tumor-derived cDNA libraries. This search
     identified 1,325 different cancer/testis-associated Unigene clusters. The
     mRNA expression pattern of 73 cancer/testis-associated
     Unigene clusters was assessed by reverse transcriptase polymerase chain
     reaction. Three gene products, CT15/Hs.177959, CT16/Hs.245431 and
     CT17/Hs.178062, were detected only in testis and in tumor tissue. CT15 is
     equivalent to ADAM2/fertilin-beta. CT16, an uncharacterized gene product,
     has homology (30-50%) to members of the GAGE gene family and is 89%
     identical to CT16.2/Hs.293317, indicating that CT16 and CT16.2 are
members
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of a new GAGE gene family. The uncharacterized gene product, CT17, has homology (30%) to phospholipase A1. RT-PCR analysis showed that CT15 is expressed exclusively in renal cancer, whereas CT16 and CT17 are expressed in a range of human cancers. Real-time RT-PCR analysis of newly defined CT genes and the prototype CT antigens, MAGE-3 and NY-ESO-1, revealed low levels (less than 3% of the level detected in testis) of CT15, CT16 and NY-ESO-1 in a limited range of normal, non-gametogenic tissues. This study demonstrates the merits of **database** mining with respect to the identification of tissue-restricted gene products expressed in cancer.

L26 ANSWER 2 OF 35 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002104309 MEDLINE
DOCUMENT NUMBER: 21644001 PubMed ID: 11784322
TITLE: Cloning and expression of sterol Delta 14-reductase from bovine liver.
AUTHOR: Roberti Rita; Bennati Anna Maria; Galli Giovanni; Caruso Donatella; Maras Bruno; Aisa Cristina; Beccari Tommaso; Della Fazia Maria Agnese; Servillo Giuseppe
CORPORATE SOURCE: Department of Internal Medicine, University of Perugia, Italy.. roberti@unipg.it
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2002 Jan) 269 (1) 283-90.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020212
Last Updated on STN: 20020222
Entered Medline: 20020221

AB Biosynthesis of cholesterol represents one of the fundamental cellular metabolic processes. Sterol Delta 14-reductase (Delta 14-SR) is a microsomal enzyme involved in the conversion of lanosterol to cholesterol in mammals. Amino-acid sequence analysis of a 38-kDa protein purified from bovine liver in our laboratory revealed > 90% similarity with a human sterol reductase, SR-1, encoded by the TM7SF2 gene, and with the C-terminal domain of human lamin B receptor. A cDNA encoding the 38-kDa protein, similar to human TM7SF2, was identified by analysis of a bovine **expressed** sequence **tag** (**EST**) **database**. The cDNA was synthesized by RT-PCR, cloned, and sequenced. The cDNA encodes a 418 amino-acid polypeptide with nine predicted transmembrane domains. The deduced amino-acid sequence exhibits high similarity with Delta 14-SR from yeasts, fungi, and plants (55-59%), suggesting that the bovine cDNA encodes Delta 14-SR. Northern blot analysis of bovine tissues showed high **expression** of **mRNA** in liver and brain. The polypeptide encoded by the cloned **cDNA** was **expressed** in COS-7 cells. Immunofluorescence analysis of transfected cells revealed a distribution of the protein throughout the ER. COS-7 cells **expressing** the **protein** exhibited Delta 14-SR activity about sevenfold higher than control cells. These results demonstrate that the cloned bovine cDNA encodes Delta 14-SR and provide evidence that the human TM7SF2 gene encodes Delta 14-SR.

L26 ANSWER 3 OF 35 CAPLUS DUPLICATE 3
ACCESSION NUMBER: 2002:158817 CAPLUS

DOCUMENT NUMBER: 136:178856
TITLE: Gene expression profiles in tadpole larvae of Ciona intestinalis
AUTHOR(S): Kusakabe, Takehiro; Yoshida, Reiko; Kawakami, Isao; Kusakabe, Rie; Mochizuki, Yasuaki; Yamada, Lixy; Shin-i, Tadasu; Kohara, Yuji; Satoh, Nori; Tsuda, Motoyuki; Satou, Yutaka
CORPORATE SOURCE: Department of Life Science, Himeji Institute of Technology, Hyogo, 678-1297, Japan
SOURCE: Developmental Biology (Orlando, FL, United States) (2002), 242(2), 188-203
CODEN: DEBIAO; ISSN: 0012-1606
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A set of 12,779 expressed sequence tags (ESTs), both the 5'-most and 3'-most ends, derived from Ciona intestinalis tadpole larvae was categorized into 3521 independent clusters, from which 1013 clusters corresponding to 9424 clones were randomly selected to analyze genetic information and gene expression profiles. When compared with sequences in databases, 545 of the clusters showed significant matches with reported proteins, while 153 showed matches with putative proteins for which there is not enough information to categorize their function, and 315 had no significant sequence similarities to known proteins. Sequence-similarity analyses of the 545 clusters in relation to the biol. functions demonstrated that 407 of them have functions that many kinds of cells use, 104 are assocd. with cell-cell communication, and 34 are transcription factors or other gene-regulatory proteins. Sequence prevalence distribution anal. demonstrated that more than one-half of the mRNAs are rare mRNAs. All of the 1013 clusters were subjected to whole-mount in situ hybridization to analyze the gene expression profile in the tadpole larva. A total of 361 clusters showed expression specific to a certain tissue or organ: 96 showed epidermis-specific expression, 60 were specific to the nervous system, 108 to endoderm, 34 to mesenchyme, 5 to trunk lateral cells, 4 to trunk ventral cells, 23 to notochord, 28 to muscle, and 3 to siphon rudiments. In addn., 190 clusters showed expression in multiple tissues. Moreover, nervous system-specific genes showed intriguing expression patterns dependent on the cluster. The present study highlights a broad spectrum of genes that are used in the formation of one of the most primitive chordate body plans as well as for the function of various types of tissue and organ and also provides mol. markers for individual tissues and organs constituting the Ciona larva. [This abstr. record is one of three records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]. (c) 2002 Academic Press.

L26 ANSWER 4 OF 35 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:94052 CAPLUS
DOCUMENT NUMBER: 136:129766
TITLE: Gene expression profile of human bone marrow stromal cells: High-throughput expressed sequence tag sequencing analysis
AUTHOR(S): Jia, Libin; Young, Marian F.; Powell, John; Yang, Liming; Ho, Nicola C.; Hotchkiss, Robert; Robey, Pamela Gehron; Francomano, Clair A.
CORPORATE SOURCE: Medical Genetics Branch, National Human Genome

Research Institute, National Institutes of Health, Bethesda, MD, 20892, USA
SOURCE: Genomics (2002), 79(1), 7-17
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Human bone marrow stromal cells (HBMSC) are pluripotent cells with the potential to differentiate into osteoblasts, chondrocytes, myelosupportive stroma, and marrow adipocytes. High-throughput DNA sequencing anal. was used to generate 4258 single-pass sequencing reactions (known as expressed sequence tags, or ESTs) obtained from the 5' (97) and 3' (4161) ends of human cDNA clones from a HBMSC cDNA library. The goal was to obtain tag sequences from the max. no. of possible genes and to deposit them in the publicly accessible database for ESTs (dbEST of the National Center for Biotechnol. Information). Comparisons of these EST sequencing data with nonredundant human mRNA and protein databases showed that the ESTs represent 1860 gene clusters. The EST sequencing data anal. showed 60 novel genes found only in this cDNA library after BLAST anal. against 3.0 million ESTs in NCBI's dbEST database. The BLAST search also showed the identified ESTs that have close homol. to known genes, which suggests that these may be newly recognized members of known gene families. The gene expression profile of this cell type is revealed by analyzing both the frequency with which a message is encountered and the functional categorization of expressed sequences. Comparing an EST sequence with the human genomic sequence database enables assignment of an EST to a specific chromosomal region (a process called digital gene localization) and often enables immediate partial detn. of intron/exon boundaries within the genomic structure. It is expected that high-throughput EST sequencing and data mining anal. will greatly promote our understanding of gene expression in these cells and of growth and development of the skeleton.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 5 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 4
ACCESSION NUMBER: 2001:106057 CAPLUS
DOCUMENT NUMBER: 134:188987
TITLE: Human expressed sequence tags and primers for synthesizing full-length cDNAs
INVENTOR(S): Ota, Toshio; Isogai, Takao; Nishikawa, Tetsuo; Hayashi, Kohji; Saito, Kaoru; Yamamoto, Junichi; Ishii, Shizuko; Sugiyama, Tomoyasu; Wakamatsu, Ai; Nagai, Keiichi; Otsuki, Tetsuji
PATENT ASSIGNEE(S): Helix Research Institute, Japan
SOURCE: Eur. Pat. Appl., 2527 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 9
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

EP 1074617	A2	20010207	EP 2000-116126	20000728
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002171977	A2	20020618	JP 2000-196309	20000626
EP 1205549	A1	20020515	EP 2000-948282	20000728
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				

PRIORITY APPLN. INFO.:

JP 1999-248036	A	19990729
JP 1999-300253	A	19990827
JP 2000-118776	A	20000111
JP 2000-183767	A	20000502
JP 2000-241899	A	20000609
US 1999-159590P	P	19991018
US 2000-183322P	P	20000217
WO 2000-JP5065	W	20000728

AB Primers for synthesizing full-length cDNAs and their use are provided. The invention provides 5'-end sequences for 5602 partial cDNA sequences (expressed sequence tags, ESTs) and 3'-end sequences for 4970 of these clones. Furthermore, primers for synthesizing the full-length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full-length cDNA sequences s of the present invention contg. the translation start site provides information useful for analyzing the functions of the proteins. Tissue- and cell-specific expression patterns are also provided. [This abstr. record is one of 6 records for this patent necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L26 ANSWER 6 OF 35 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 2001648417 MEDLINE
DOCUMENT NUMBER: 21548931 PubMed ID: 11691810
TITLE: Tumor antigens isolated from a patient with vitiligo and T-cell-infiltrated melanoma.
AUTHOR: Kiniwa Y; Fujita T; Akada M; Ito K; Shofuda T; Suzuki Y; Yamamoto A; Saida T; Kawakami Y
CORPORATE SOURCE: Division of Cellular Signaling, Institute for Advanced Medical Research, Keio University School of Medicine, Tokyo 160-8582, Japan.
SOURCE: CANCER RESEARCH, (2001 Nov 1) 61 (21) 7900-7. Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011112
Last Updated on STN: 20020123
Entered Medline: 20011204

AB Serological identification of tumor antigens by **cDNA expression** cloning is a technique used to isolate cDNAs encoding tumor antigens that are recognized by IgG antibodies in sera from cancer patients. It is also useful for the isolation of tumor antigens recognized by T cells. We applied this method to identify melanoma antigens recognized by the serum from a patient with a good prognosis who had T-cell-infiltrated melanoma and vitiligo. By screening a lambda phage cDNA library constructed from a highly pigmented melanoma cell line, SKmel23, with the patient's serum, 50 positive cDNA clones consisting of 26 distinct antigens were isolated. Of these, 20 encoded known proteins, and

6 encoded previously uncharacterized ones. The most frequently isolated clone, which we named KU-MEL-1, was unknown previously but was homologous to partial cDNA sequences registered in the **expressed** sequence **tag database**. Reverse transcription-PCR and Northern blot analysis demonstrated that KU-MEL-1 was strongly expressed in most melanoma cell lines, melanoma tissue samples, and cultured melanocytes and weakly expressed in cell lines derived from other types of tumors, as well as in some normal tissues, including testis. Western blot analysis with polyclonal murine antibody generated by immunization with the recombinant KU-MEL-1 protein demonstrated that the KU-MEL-1 **protein** was preferentially **expressed** in melanoma cells and melanocytes. IgG antibodies against KU-MEL-1 were detected in the sera from 9 of 26 melanoma patients and from some patients with other cancers, including brain tumor, esophageal cancer, colon cancer, and chronic myelogenous leukemia, but were not detected in sera from 30 healthy individuals. Although the IgG specific for KU-MEL-1 was not detected in sera from 12 vitiligo patients, it was detected in sera from 7 of 11 patients with Vogt-Koyanagi-Harada disease that is thought to be an autoimmune disease against melanocytes. These results suggest that KU-MEL-1 may be a useful target for the development of diagnostic and therapeutic methods for patients with various cancers, particularly with melanoma, as well as patients with autoimmune diseases against melanocytes.

L26 ANSWER 7 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 6
ACCESSION NUMBER: 2002:79219 CAPLUS
DOCUMENT NUMBER: 136:97064
TITLE: Gene expression in the developing mouse retina by EST sequencing and microarray analysis
AUTHOR(S): Mu, Xiuqian; Zhao, Sheng; Pershad, Rashmi; Hsieh, Tzung-Fu; Scarpa, Ann; Wang, Steven W.; White, R. Allen; Beremand, Phillip D.; Thomas, Terry L.; Gan, Lin; Klein, William H.
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, The University of Texas M. D. Anderson Cancer Center, Houston, 77030, USA
SOURCE: Nucleic Acids Research (2001), 29(24), 4983-4993
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Retinal development occurs in mice between embryonic day E11.5 and post-natal day P8 as uncommitted neuroblasts assume retinal cell fates. The genetic pathways regulating retinal development are being identified but little is understood about the global networks that link these pathways together or the complexity of the expressed gene set required to form the retina. At E14.5, the retina contains mostly uncommitted neuroblasts and newly differentiated neurons. This report describes a sequence anal. of an E14.5 retinal cDNA library. To date, 15,268 ESTs have been archived and 9035 have been annotated, which represent 5288 genes. The fraction of singly occurring ESTs as a function of total EST accrual suggests that the total no. of expressed genes in the library could approach 27,000. The 9035 ESTs were categorized by their known or putative functions. Representation of the genes involved in eye development was significantly higher in the retinal clone set compared with the NIA mouse 15K cDNA clone set. Screening with a microarray contg. 864 cDNA clones using wild-type and brn-3b (-/-) retinal cDNA probes revealed a potential regulatory linkage between the transcription factor Brn-3b and expression of GAP-43, a protein assocd. with axon growth. The

retinal EST database will be a valuable platform for gene expression profiling and a new source for gene discovery; the ESTs are deposited in GenBank with Accession Nos. BG799964-BG808997 and BI985056-BI991757. [This abstr. record is one of three records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L26 ANSWER 8 OF 35 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001389170 MEDLINE
DOCUMENT NUMBER: 21336737 PubMed ID: 11443211
TITLE: Expression of reduced nicotinamide adenine dinucleotide phosphate oxidase (ThoX, LNOX, Duox) genes and proteins in human thyroid tissues.
AUTHOR: Caillou B; Dupuy C; Lacroix L; Nocera M; Talbot M; Ohayon R; Deme D; Bidart J M; Schlumberger M; Virion A
CORPORATE SOURCE: Department of Pathology, Institut Gustave-Roussy, 94805 Villejuif, France.
SOURCE: JOURNAL OF CLINICAL ENDOCRINOLOGY AND METABOLISM, (2001 Jul) 86 (7) 3351-8.
Journal code: 0375362. ISSN: 0021-972X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

AB The large homolog of NADPH oxidase flavoprotein LNOX2, and probably LNOX1, are flavoproteins involved in the thyroid H(2)O(2) generator. Western blot analysis of membrane proteins from normal human thyroid, using antipeptide antibodies, indicated that LNOX1,2 are 164-kDa glycoproteins and that N-glycosylated motifs account for at least 10-20 kDa of their total apparent molecular mass. Northern blot analysis of 23 different human tissues demonstrated that LNOX2 messenger RNA (**mRNA**) is strongly **expressed** only in the thyroid gland, although blast analysis of **expressed** sequence **tags databases** indicated that LNOX genes are also expressed in some nonthyroid cells. We investigated LNOX1,2 gene and **protein expressions** in normal and pathological human thyroid tissues using real-time kinetic quantitative PCR and antipeptide antibodies, respectively. In normal tissue, LNOX1,2 are localized at the apical pole of thyrocytes. Immunostaining for LNOX1,2 was heterogeneous, inside a given follicle, with 40-60% of positive follicular cells. Among normal and pathological tissues, variations of LNOX1 and LNOX2 mRNA levels were parallel, suggesting a similar regulation of both gene **expressions**. Whereas LNOX **mRNAs** seemed slightly affected in benign disease, the **expression** of **protein** was highly variable. In multinodular goiters, 40-60% of cells were stained. In hypofunctioning adenomas, LNOX immunostaining was highly variable among follicles, whereas sodium/iodide (Na+/I-) symporter immunostaining was decreased. In hyperfunctioning thyroid tissues, only few cells (0-10%) were weakly stained, whereas sodium/iodide symporter staining was found in the majority of follicular cells. In conclusion, LNOX proteins are new apical glycoproteins with a regulation of expression that differs from other

thyroid markers.

L26 ANSWER 9 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 8
ACCESSION NUMBER: 2001:649893 CAPLUS
DOCUMENT NUMBER: 135:176297
TITLE: Gene expression profiles in Ciona intestinalis tailbud embryos
AUTHOR(S): Satou, Yutaka; Takatori, Naohito; Yamada, Lixy; Mochizuki, Yasuaki; Hamaguchi, Makoto; Ishikawa, Hisayoshi; Chiba, Shota; Imai, Kaoru; Kano, Shungo; Murakami, Seiko D.; Nakayama, Akie; Nishino, Atsuo; Sasakura, Yasunori; Satoh, Gohki; Shimotori, Taishin; Shin-i, Tadasu; Shoguchi, Eiichi; Suzuki, Miho M.; Takada, Norio; Utsumi, Nanami; Yoshida, Natsue; Saiga, Hidetoshi; Kohara, Yuji; Satoh, Nori
CORPORATE SOURCE: Department of Zoology, Graduate School of Science, Kyoto University, Kyoto, 606-8502, Japan
SOURCE: Development (Cambridge, United Kingdom) (2001), 128(15), 2893-2904
CODEN: DEVPED; ISSN: 0950-1991
PUBLISHER: Company of Biologists Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A set of 3423 expressed sequence tags derived from the Ciona intestinalis tailbud embryos was categorized into 1213 independent clusters. When compared with DNA Data Bank of Japan database, 502 clusters of them showed significant matches to reported proteins with distinct function, whereas 184 lacked sufficient information to be categorized (including reported proteins with undefined function) and 527 had no significant similarities to known proteins. Sequence similarity analyses of the 502 clusters in relation to the biosynthetic function, as well as the structure of the message population at this stage, demonstrated that 390 of them were assocd. with functions that many kinds of cells use, 85 with cell-cell communication and 27 with transcription factors and other gene regulatory proteins. All of the 1213 clusters were subjected to whole-mount in situ hybridization to analyze the gene expression profiles at this stage. A total of 387 clusters showed expression specific to a certain tissue or organ; 149 showed epidermis-specific expression; 34 were specific to the nervous system; 29 to endoderm; 112 to mesenchyme; 32 to notochord; and 31 to muscle. Many genes were also specifically expressed in multiple tissues. The study also highlighted characteristic gene expression profiles dependent on the tissues. In addn., several genes showed intriguing expression patterns that have not been reported previously; for example, four genes were expressed specifically in the nerve cord cells and one gene was expressed only in the posterior part of muscle cells. This study provides mol. markers for each of the tissues and/or organs that constitutes the Ciona tailbud embryo. The sequence information will also be used for further genome scientific approach to explore mol. mechanisms involved in the formation of one of the most primitive chordate body plans. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L26 ANSWER 10 OF 35 MEDLINE DUPLICATE 9

ACCESSION NUMBER: 2001213322 MEDLINE
DOCUMENT NUMBER: 21103328 PubMed ID: 11160356
TITLE: Isolation of a new melanoma antigen, MART-2, containing a mutated epitope recognized by autologous tumor-infiltrating T lymphocytes.
AUTHOR: Kawakami Y; Wang X; Shofuda T; Sumimoto H; Tupesis J; Fitzgerald E; Rosenberg S
CORPORATE SOURCE: Division of Cellular Signaling, Institute for Advanced Medical Research, Keio University School of Medicine, Tokyo, Japan.. yutakawa@med.keio.ac.jp
SOURCE: JOURNAL OF IMMUNOLOGY, (2001 Feb 15) 166 (4) 2871-7. Journal code: 2985117R. ISSN: 0022-1767.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010425
Last Updated on STN: 20010425
Entered Medline: 20010419

AB Using **cDNA expression** cloning, a **cDNA** encoding a novel human melanoma Ag, MART-2 (melanoma Ag recognized by T cells-2), recognized by HLA-A1-restricted CD8(+) T cells from tumor-infiltrating lymphocytes (TIL1362) was isolated from an autologous melanoma cell line, 1362 mel. Homologous sequences to the cDNA had been registered in the **EST database**. This gene encoded an uncharacterized **protein expressed** ubiquitously in most normal and cancer cells. A mutation (A to G transition) was found in the cDNA obtained from the1362 mel melanoma cell line in the sequences encoding the phosphate binding loop (P-loop) that resulted in loss of the ability to bind GTP. Transfection of NIH-3T3 with the mutated MART-2 did not result in the development of significant foci. By screening 36 various cancer cell lines using single-strand conformation polymorphism, a possible mutation in the P-loop of MART-2 was found in one squamous cell lung cancer cell line, EBC1. The T cell epitope for TIL1362, FLEGNEVGKTY, was identified to be encoded by the mutated sequence of the MART-2 Ag. The mutation substituted glycine in the normal peptide with glutamic acid at the third amino acid of the epitope, which is an important primary anchor amino acid for HLA-A1 peptide binding. The normal peptide, FLGGNEVGKTY, was not recognized by TIL1362, suggesting that this T cell response was specific for the autologous tumor. Although transforming activity was not detected in the NIH-3T3 assay, MART-2 with the mutation in the P-loop may be involved in the generation of melanoma through a loss of GTP binding activity.

L26 ANSWER 11 OF 35 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2001210657 MEDLINE
DOCUMENT NUMBER: 21196070 PubMed ID: 11299361
TITLE: ANT1, an aromatic and neutral amino acid transporter in Arabidopsis.
AUTHOR: Chen L; Ortiz-Lopez A; Jung A; Bush D R
CORPORATE SOURCE: Program in Physiological and Molecular Plant Biology, Urbana, Illinois 61801.
SOURCE: PLANT PHYSIOLOGY, (2001 Apr) 125 (4) 1813-20. Journal code: 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

AB A new amino acid transporter was identified from the Arabidopsis **expressed** sequence **tag cDNAs** by **expressing** the **cDNA** in a yeast amino acid transport mutant. Transport analysis of the **expressed protein** in yeast showed that it transports aromatic and neutral amino acids, as well as arginine. This transporter (ANT1, aromatic and neutral transporter) also transports indole-3-acetic acid and 2,4-dichlorophenoxyacetic acid. The cDNA is 1.6 kb in length with an open reading frame that codes for a protein with 432 amino acids and a calculated molecular mass of 50 kD. Hydropathy analysis showed ANT1 is an integral membrane protein with 11 putative membrane-spanning domains. Southern analysis and a BLAST search of the Arabidopsis genome **database** suggests that ANT1 is part of a small gene family containing at least five members. Phylogenetic comparisons with other known amino acid transporters in plants suggests that ANT1 represents a new class of amino acid transporter. RNA gel-blot analysis showed that this transporter is expressed in all organs with highest abundance in flowers and cauline leaves.

L26 ANSWER 12 OF 35 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 2001:65218 LIFESCI
TITLE: ANT1, an Aromatic and Neutral Amino Acid Transporter in Arabidopsis
AUTHOR: Chen, L.; Ortiz-Lopez, A.; Jung, A.; Bush*, D.R.
CORPORATE SOURCE: Program in Physiological and Molecular Plant Biology, United States Department of Agriculture-Agricultural Research Service; E-mail: dbush@uiuc.edu
SOURCE: Plant Physiology [Plant Physiol.], (20010300) vol. 125, no.
3, pp. 1813-1820.
ISSN: 0032-0889.
DOCUMENT TYPE: Journal
FILE SEGMENT: G
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A new amino acid transporter was identified from the Arabidopsis **expressed** sequence **tag cDNAs** by **expressing** the **cDNA** in a yeast amino acid transport mutant. Transport analysis of the **expressed protein** in yeast showed that it transports aromatic and neutral amino acids, as well as arginine. This transporter (ANT1, aromatic and neutral transporter) also transports indole-3-acetic acid and 2,4-dichlorophenoxyacetic acid. The cDNA is 1.6 kb in length with an open reading frame that codes for a protein with 432 amino acids and a calculated molecular mass of 50 kD. Hydropathy analysis showed ANT1 is an integral membrane protein with 11 putative membrane-spanning domains. Southern analysis and a BLAST search of the Arabidopsis genome **database** suggests that ANT1 is part of a small gene family containing at least five members. Phylogenetic comparisons with other known amino acid transporters in plants suggests that ANT1 represents a new class of amino acid transporter. RNA gel-blot analysis showed that this transporter is expressed in all organs with highest abundance in flowers and cauline leaves.

L26 ANSWER 13 OF 35 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 2002036073 MEDLINE
DOCUMENT NUMBER: 21604065 PubMed ID: 11763134
TITLE: Analysis of genes expressed during rice-Magnaporthe grisea

interactions.

AUTHOR: Kim S; Ahn I P; Lee Y H

CORPORATE SOURCE: School of Agricultural Biotechnology and Research Center for New Bio-Materials in Agriculture, Seoul National University, Suwon, Korea.

SOURCE: MOLECULAR PLANT-MICROBE INTERACTIONS, (2001 Nov) 14 (11) 1340-6.
Journal code: 9107902. ISSN: 0894-0282.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200206

ENTRY DATE: Entered STN: 20020124
Last Updated on STN: 20020604
Entered Medline: 20020603

AB **Expressed** sequence **tag** (**EST**) analysis was applied to identify rice genes involved in defense responses against infection by the blast fungus Magnaporthe grisea and fungal genes involved in growth within the host during a compatible interaction. A total of 511 clones was sequenced from a cDNA library constructed from rice leaves (Oryza sativa cv. Nipponbare) infected with M. grisea strain 70-15 to generate 296 nonredundant **ESTs**. The sequences of 293 clones (57.3%) significantly matched National Center for Biotechnology Information **database** entries; 221 showed homologies with previously identified plant genes and 72 with fungal genes. Among the genes with assigned functions, 32.8% were associated with metabolism, 29.4% with cell/organism defense or pathogenicity, and 18.4% with gene/**protein expression**. **cDNAs** encoding a type I metallothionein (MTs-1) of rice and a homolog of glucose-repressible gene 1 (GRG1) of Neurospora crassa were the most abundant representatives of plant and fungal genes, comprising 2.9 and 1.6% of the total clones, respectively. The expression patterns of 10 **ESTs**, five each from rice and M. grisea, were analyzed. Five defense-related genes in rice, including four pathogenesis-related genes and MTs-1, were highly expressed during M. grisea infection. Expression of five stress-inducible or pathogenicity-related genes of the fungus, including two hydrophobin genes, was also induced during growth within the host. Further characterization of the genes represented in this study would be an aid in unraveling the mechanisms of pathogenicity of M. grisea and the defense responses of rice.

L26 ANSWER 14 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 12

ACCESSION NUMBER: 2001:530716 CAPLUS

DOCUMENT NUMBER: 135:314145

TITLE: Creation of genome-wide protein expression libraries using random activation of gene expression

AUTHOR(S): Harrington, John J.; Sherf, Bruce; Rundlett, Stephen; Jackson, P. David; Perry, Rob; Cain, Scott; Leventhal, Christina; Thornton, Mark; Ramachandran, Rakesh; Whittington, Jessica; Lerner, Laura; Costanzo, Dana; McElligott, Karen; Boozer, Sherry; Mays, Robert; Smith, Emery; Veloso, Neil; Klika, Alison; Hess, Jennifer; Cothren, Kevin; Lo, Kalok; Offenbacher, Jason; Danzig, Joel; Ducar, Matt

CORPORATE SOURCE: Athersys, Inc., Cleveland, OH, 44115, USA

SOURCE: Nature Biotechnology (2001), 19(5), 440-445

CODEN: NABIF9; ISSN: 1087-0156
PUBLISHER: Nature America Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Random activation of gene expression (RAGE) can be used to create genome-wide protein expression libraries. RAGE libraries contg. only 5 .times. 106 individual clones were found to express every gene tested, including genes that are normally silent in the parent cell line. Furthermore, endogenous genes were activated at similar frequencies and expressed at similar levels within RAGE libraries created from multiple human cell lines, demonstrating that RAGE libraries are inherently normalized. Pools of RAGE clones were used to isolate 19,547 human gene clusters, .apprx.53% of which were novel when tested against public databases of expressed sequence tag (EST) and complementary DNA (cDNA). Isolation of individual clones confirmed that the activated endogenous genes can be expressed at high levels to produce biol. active proteins. The properties of RAGE libraries and RAGE expression clones are well suited for a no. of biotechnol. applications including gene discovery, protein characterization, drug development, and protein manufg. The sequences are available in the GenBank database with Accession Nos. BG181162-BG222060, BG227959-BG228009,BG459627-BG462150, and BG466129. [This abstr. record is one of 11 records for this document necessitated by the large no. of index entries required to fully index the document and publication constraints.].

L26 ANSWER 15 OF 35 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 2002158014 MEDLINE
DOCUMENT NUMBER: 21888117 PubMed ID: 11891679
TITLE: Comprehensive resource: Skeletal gene database.
AUTHOR: Jia L; Ho N C; Park S S; Powell J; Francomano C A
CORPORATE SOURCE: MGB/NHGRI/NIH Rockville, MD 20892, USA..
libinj2@mail.nih.gov
SOURCE: AMERICAN JOURNAL OF MEDICAL GENETICS, (2001 Winter) 106 (4) 275-81.
Journal code: 7708900. ISSN: 0148-7299.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020606
Entered Medline: 20020605
AB The Skeletal Gene **Database** (SGD) is an integrated resource that provides comprehensive information about bone-related genes, **mRNA**, and **proteins expressed** in human and mouse, with rich links to numerous other electronic tools. SGD contains **expressed** sequence **tag** (**EST**) data from all the skeletal-related cDNA libraries that are available to the public. It supplies the query/data access analytic tools for users to search and compare each gene expressed in skeletal tissue(s). The results derived from **EST** tissue expression profiling will allow users to get the data on the mRNA copy numbers of each gene expressed in each tissue and its normalized value. From the SGD, researchers can obtain information regarding the name, symbol, size, exon/intron number, chromosomal location, LocusLink, and related disease (if any is known) of each gene. This electronic compendium also furnishes information on the protein of the corresponding gene including the protein size (amino acid number and molecular weight).

It provides swift and ready access to other useful **databases** including OMIM, UniGene and PUBMED. The data will be updated regularly in step with current and future research, thereby providing what we hope will serve as a highly useful source of information and a powerful analytic tool to the scientific community.

L26 ANSWER 16 OF 35 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:430970 CAPLUS
DOCUMENT NUMBER: 136:113549
TITLE: In silico mining of EST databases for novel pre-implantation embryo-specific zinc finger protein genes
AUTHOR(S): Choo, Kong-Bung; Chen, Huang-Hui; Cheng, Winston T. K.; Chang, Hung-Shue; Wang, Manni
CORPORATE SOURCE: Recombinant DNA Laboratory, Department of Medical Research and Education, Veterans General Hospital-Taipei, Taipei, 11217, Taiwan
SOURCE: Molecular Reproduction and Development (2001), 59(3), 249-255
CODEN: MREDEE; ISSN: 1040-452X
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Progress in the understanding of early mammalian embryo development has been severely hampered by scarcity of study materials. To circumvent such a constraint, we have developed a strategy that involves a combination of in silico mining of new genes from expressed sequence tags (EST) databases and rapid detn. of expression profiles of the dbEST-derived genes using a PCR-based assay and a panel of cDNA libraries derived from different developmental stages and somatic tissues. We demonstrate that in a random sample of 49 independent dbEST-derived zinc finger protein genes mined from a mouse embryonic 2-cell cDNA library, more than three-quarters of these genes are novel. Examn. of characteristics of the human orthologues derived from these mouse genes reveals that many of them are assocd. with human malignancies. Expression studies have further led to the identification of three novel genes that are exclusively expressed in mouse embryos before or up to the 8-cell stage. Two of the genes, designated 2czf45 and 2czf48 (2czf for 2-cell zinc finger), are zinc finger protein genes coding for a RBCC protein with a RFP domain and a protein with three C2H2 fingers, resp. The third gene, designated 2cpoz56, codes for a protein with a POZ domain that is often assocd. with zinc finger proteins. These three genes are candidate genes for regulatory or other functions in early embryogenesis. The strategy described in this report should generally be applicable to rapid and large-scale mining of other classes of rare genes involved in other biol. and pathol. processes.
REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 17 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 14
ACCESSION NUMBER: 2000:576912 CAPLUS
DOCUMENT NUMBER: 133:160371
TITLE: Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental

cDNA microarray
AUTHOR(S): Tanaka, Tetsuya S.; Jarada, Saied A.; Lim, Meng K.; Kargul, George J.; Wang, Xiaohong; Grahovac, ,Marija J.; Pantano, Serafino; Sano, Yuri; Piao, Yulan; Nagaraja, Ramaiah; Doi, Hirofumi; Wood, William H., III; Becker, Kevin, G.; Ko, Minoru S. H.
CORPORATE SOURCE: Laboratory of Genetics, National Institutes of Health,
Baltimore, MD, 21224-5820, USA
SOURCE: Proceedings of the National Academy of Sciences of the
United States of America (2000), 97(16), 9127-9132
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Complementary DNA microarray technol. has been increasingly used to monitor global gene expression patterns in various tissues and cell types.
However, applications to mammalian development have been hampered by the lack of appropriate cDNA collections, particularly for early developmental
stages. To overcome this problem, a PCR-based cDNA library construction method was used to derive 52,374 expressed sequence tags from pre- and peri-implantation embryos, embryonic day (E) 12.5 female gonad/mesonephros, and newborn ovary. From these cDNA collections, a microarray representing 15,264 unique genes (78% novel and 22% known) was assembled. In initial applications, the divergence of placental and embryonic gene expression profiles was assessed. At stage E12.5 of development, based on triplicate expts., 720 genes (6.5%) displayed statistically significant differences in expression between placenta and embryo. Among 289 more highly expressed in placenta, 61 placenta-specific
genes encoded, for example, a novel prolactin-like protein. The no. of genes highly expressed (and frequently specific) for placenta has thereby been increased 5-fold over the total previously reported, illustrating the
potential of the microarrays for tissue-specific gene discovery and anal. of mammalian developmental programs. The sequences of the expressed sequence tags are available in the GenBank database at Accession Nos. AW537829-AW545916, AW535144-AW537732, AW545922-AW559162, and AF272368. [This abstr. record is one of 6 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L26 ANSWER 18 OF 35 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2000-06824 BIOTECHDS
TITLE: PPMdb: a plant plasma membrane database; Arabidopsis thaliana proteome database; goals and applications
AUTHOR: Sahnoun I; Dehais P; van Montagu M; Rossignol M; *Rouze P
CORPORATE SOURCE: Univ.Ghent; Flanders-Inst.Biotechnol.; INRA; CNRS; ENSA
LOCATION: Laboratoire Associe de l'Institut de la Recherche Agronomique
(France), Department of Plant Genetics, University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium.
Email: pirou@gengenp.rug.ac.be
SOURCE: J.Biotechnol.; (2000) 78, 3, 235-46
CODEN: JBITD4
ISSN: 0168-1656
DOCUMENT TYPE: Journal

LANGUAGE: English
AN 2000-06824 BIOTECHDS
AB PPMdb is a proteome **database** dedicated to proteins from plant plasma membranes. Its goals are: (1) to provide comprehensive 2-dimensional PAGE maps of plasma membrane proteins of Arabidopsis thaliana; (2) to characterize their expression patterns under defined conditions and in various tissues; (3) to obtain partial amino acid sequence information on these plasma membrane proteins; and (4) to associate **protein expression** and sequence data with available **expressed** sequence **tags** (**ESTs**) and, in the near future, with microarray **mRNA** **expression** data. The choice has been made to focus on plasma membrane proteins because: (1) they play a role in major plant cellular processes, such as biological and chemical environment sensing, signal transduction, and transport of molecules; and (2) plasma membrane proteins have been poorly characterized within the existing proteomic **databases**. All information is gathered and structured in a relational **database**, after being analyzed and annotated. PPMdb includes active links to related biological **databases**, and users can query the **database** by accession number, protein name, pI, mol.wt. and cellular location. (13 ref)

L26 ANSWER 19 OF 35 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 2000395635 MEDLINE
DOCUMENT NUMBER: 20323158 PubMed ID: 10864470
TITLE: Gpbox (Psx2), a homeobox gene preferentially expressed in female germ cells at the onset of sexual dimorphism in mice.
AUTHOR: Takasaki N; McIsaac R; Dean J
CORPORATE SOURCE: Laboratory of Cellular and Developmental Biology, NIDDK, National Institutes of Health, Bethesda, Maryland 20892, USA.
SOURCE: DEVELOPMENTAL BIOLOGY, (2000 Jul 1) 223 (1) 181-93.
Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000811

AB XX gonads differentiate into ovaries, a morphologic event evident by embryonic day 13.5 (E13.5) in mice. To identify early markers of oogenesis, sex-specific urogenital ridge cDNA libraries were constructed from E12-13 embryos. After mass excision and isolation of plasmid DNA, approximately 4800 **expressed** sequence **tags** were determined and compared to existing **databases**. Few **cDNAs** were specifically **expressed** in the urogenital ridge, but one, designated GPBOX, encodes a 227-amino-acid homeobox **protein** that is first **expressed** at E10.5 in the embryo as well as in the extraembryonic tissues. The Gpbox gene is single copy in the mouse genome and is located on the X chromosome in close proximity to two other homeobox genes, Pem and Psx1. Within the embryo, its expression is limited to the gonad, and transcripts are not detected in adult tissues. Although comparable levels are initially present in both sexes, GPBOX transcripts accumulate faster in female germ cells and peak at E12.5 when they are present in fivefold greater abundance than in males. The persistence of GPBOX transcripts in female germ cells until E15.5 and their virtual disappearance in males by E13.5 suggest that Gpbox may play a role in

mammalian oogenesis.
Copyright 2000 Academic Press.

L26 ANSWER 20 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 16
ACCESSION NUMBER: 2000:527731 CAPLUS
DOCUMENT NUMBER: 133:160368
TITLE: A large scale analysis of cDNA in Arabidopsis thaliana: generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
AUTHOR(S): Asamizu, Erika; Nakamura, Yasukazu; Sato, Shusei; Tabata, Satoshi
CORPORATE SOURCE: Kazusa DNA Research Institute, Chiba, 292-0812, Japan
SOURCE: DNA Research (2000), 7(3), 175-180
CODEN: DARSE8; ISSN: 1340-2838
PUBLISHER: Universal Academy Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB For comprehensive anal. of genes expressed in the model dicotyledonous plant, Arabidopsis thaliana, expressed sequence tags (ESTs) were accumulated. Normalized and size-selected cDNA libraries were constructed from aboveground organs, flower buds, roots, green siliques and liq.-cultured seedlings, resp., and a total of 14,026 5'-end ESTs and 39,207 3'-end ESTs were obtained. The 3'-end ESTs could be clustered into 12,028 non-redundant groups. Similarity search of the non-redundant ESTs against the public non-redundant protein database indicated that 4816 groups show similarity to genes of known function, 1864 to hypothetical genes, and the remaining 5348 are novel sequences. Gene coverage by the non-redundant ESTs was analyzed using the annotated genomic sequences of .apprx.10 Mb on chromosomes 3 and 5. A total of 923 regions were hit by at least one EST, among which only 499 regions were hit by the ESTs deposited in the public database. The result indicates that the EST source generated in this project complements the EST data in the public database and facilitates new gene discovery. The EST sequences reported in this document appear in the GenBank databank with accession nos. AB038710-AB038726, AV439465-AV442830 and AV517879-AV567728, and at the web site http://www.kazusa.or.jp/en/plant/arabi/EST/. [This abstr. record is one of 11 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L26 ANSWER 21 OF 35 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 2000400695 MEDLINE
DOCUMENT NUMBER: 20371174 PubMed ID: 10908795
TITLE: High-throughput protein expression of cDNA products as a tool in functional genomics.
AUTHOR: Larsson M; Graslund S; Yuan L; Brundell E; Uhlen M; Hoog C; Stahl S
CORPORATE SOURCE: Department of Biotechnology, Royal Institute of Technology, S-100 44, Stockholm, Sweden.
SOURCE: JOURNAL OF BIOTECHNOLOGY, (2000 Jun 23) 80 (2) 143-57.
Journal code: 8411927. ISSN: 0168-1656.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000901
Last Updated on STN: 20000901
Entered Medline: 20000824

AB A proteomics approach has been developed aimed to allow high throughput analysis of **protein** products **expressed** from **cDNA** fragments (**expressed** sequence **tags**, **ESTs**). The concept relies on expression of gene products to generate specific antibodies for protein analysis, such as immunolocalization of the proteins on cellular and subcellular level. To evaluate the system, 55 cDNA clones with predominantly unknown function were selected from a mouse testis **cDNA**-library. A bacterial **expression** system was designed that allowed robust **expression** and easy purification. **Protein** levels between 15 and 80 mg l(-1) were obtained for 49 of the clones. Five clones were selected for immunization and all yielded functional antibodies that gave specific staining in Western blot screening of samples from various cell types. Furthermore, extensive immunolocalization information on subcellular level was obtained for three of the five clones. All generated data were stored in a relational **database**, and are made available through a web-interface (http://www.biochem.kth.se/multiscale/), which also provides relevant links and allows homology searches from the original sequences. The possibility to allow analysis of gene products from whole genomes using this 'localization proteomics' approach is discussed.

L26 ANSWER 22 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 18
ACCESSION NUMBER: 2000:516432 CAPLUS
DOCUMENT NUMBER: 133:100257
TITLE: Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
AUTHOR(S): Asamizu, Erika; Nakamura, Yasukazu; Sato, Shusei; Tabata, Satoshi
CORPORATE SOURCE: Kazusa DNA Research Institute, Chiba, 292-0812, Japan
SOURCE: DNA Research (2000), 7(2), 127-130
CODEN: DARSE8; ISSN: 1340-2838
PUBLISHER: Universal Academy Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB For comprehensive anal. of genes expressed in a model legume, Lotus japonicus, a total of 22,983 5'-end expressed sequence tags (ESTs) were accumulated from normalized and size-selected cDNA libraries constructed from young (2-wk-old) plants. The EST sequences were clustered into 7137 non-redundant groups. Similarity search against public non-redundant protein database indicated that 3302 groups showed similarity to genes of known function, 1143 groups to hypothetical genes, and 2692 were novel sequences. Homologs of 5 nodule-specific genes which have been reported in other legume species were contained in the collected ESTs, suggesting that the EST source generated in this study will become a useful tool for identification of genes related to legume-specific biol. processes. The sequence data of individual ESTs are available at the web site: http://www.kazusa.or.jp/en/plant/lotus/EST/ and GenBank Accession Nos. AV406328-AV429310. [This abstr. record is the fourth of 5 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L26 ANSWER 23 OF 35 MEDLINE DUPLICATE 19

ACCESSION NUMBER: 2000334233 MEDLINE
DOCUMENT NUMBER: 20334233 PubMed ID: 10873568
TITLE: Characterization of novel and identified genes in guinea pig organ of corti.
AUTHOR: Oshima T; Nakajima T; Wada H; Ikeda K; Takasaka T
CORPORATE SOURCE: Department of Otorhinolaryngology, Tohoku University School of Medicine, 1-1 Seiryo-machi, Aoba-ku, Sendai, 980-8574, Japan.. oshima@orl.med.tohoku.ac.jp
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Jun 24) 273 (1) 84-9.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AU081352; GENBANK-AU081353; GENBANK-AU081354; GENBANK-AU081355; GENBANK-AU081356; GENBANK-AU081357; GENBANK-AU081358; GENBANK-AU081359; GENBANK-AU081360; GENBANK-AU081361; GENBANK-AU081362; GENBANK-AU081363; GENBANK-AU081364; GENBANK-AU081365; GENBANK-AU081366; GENBANK-AU081367; GENBANK-AU081368; GENBANK-AU081369; GENBANK-AU081370; GENBANK-AU081371; GENBANK-AU081372; GENBANK-AU081373; GENBANK-AU081374; GENBANK-AU081375; GENBANK-AU081376; GENBANK-AU081377; GENBANK-AU081378; GENBANK-AU081379; GENBANK-AU081380; GENBANK-AU081381; +
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000810
Last Updated on STN: 20000810
Entered Medline: 20000727

AB A number of **proteins** are **expressed** in the organ of Corti and are considered to be responsible for hearing. However, most of them have not been identified. Therefore, to achieve a better understanding of the genetic factors influencing these traits, the first step is to characterize the genes expressed in the organ of Corti. In the present study, a cDNA library was constructed from the guinea pig organ of Corti. After sequencing isolated clones, 196 **expressed** sequence **tags** (**ESTs**) were identified with FASTA analysis: 65 **ESTs** showed significant sequence homology to previously identified genes in guinea pig, human or other species, and 131 **ESTs** showed no significant matches to sequences already present in the DNA **database** DDBJ/GenBank/EMBL. A variety of matching sequences, some of which were known to be cochlea-specific, were found through FASTA analysis of the 65 clones. RT-PCR with a panel of 10 different tissue **mRNA** revealed the restricted **expression** of 13 unknown clones. The results of our analysis allowed the establishment of a list of genes expressed in the guinea pig organ of Corti.

L26 ANSWER 24 OF 35 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 2000163500 MEDLINE
DOCUMENT NUMBER: 20163500 PubMed ID: 10701565
TITLE: Analysis of messages expressed by Echinostoma paraensei miracidia and sporocysts, obtained by random EST sequencing.
AUTHOR: Adema C M; Leonard P M; DeJong R J; Day H L; Edwards D J; Burgett G; Hertel L A; Loker E S
CORPORATE SOURCE: Department of Biology, University of New Mexico, Albuquerque 87131, USA.

CONTRACT NUMBER: AI24340 (NIAID)
SOURCE: JOURNAL OF PARASITOLOGY, (2000 Feb) 86 (1) 60-5.
Journal code: 7803124. ISSN: 0022-3395.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200003
ENTRY DATE: Entered STN: 20000327
Last Updated on STN: 20000327
Entered Medline: 20000313

AB A lambdaZAP **Express cDNA** library was constructed with mRNA obtained from immature miracidia within eggs, hatched miracidia, and sporocysts of Echinostoma paraensei. This cDNA library was amplified and 213 **expressed** sequence **tag** (**EST**) sequences (averaging 466 nucleotides in length) were obtained. The mean percentage of unresolved bases within the **EST** sequences was 0.4%, ranging from 0 to 4.6%. The 213 **ESTs** represent 151 unique messages. BLAST (version 2.0.8) analysis disclosed that 64 unique E. paraensei messages (42.4%) had significant similarities (BLAST score < or =e-5), at deduced amino acid or nucleotide levels, with known sequences in the nonredundant GenBank **databases** or the dbEST **database** (NCBI). The remainder, 57.6% of the unique **EST**-encoded messages, scored nonsignificant hits. Most of the E. paraensei messages that could be assigned a cellular role based on sequence similarities were involved in gene/**protein expression**. Several **ESTs** scored highest similarities with sequences obtained from trematode species. A total of 22,560 nucleotides present in open reading frames from **ESTs** that aligned with known sequences was used to determine codon usage for E. paraensei. Analysis of a subset of eight **ESTs** that contained full-length open reading frames did not reveal a bias in codon usage. Also, **EST** sequences were found to contain 3' untranslated regions with an average length of 69.9 +/- 88.4 nucleotides (n = 46). The **EST** sequences were submitted to GenBank/dbEST, adding to the 51 available Echinostoma-derived sequences, to provide reference information for both phylogenetic analysis and study of general trematode biology.

L26 ANSWER 25 OF 35 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 1999238449 MEDLINE
DOCUMENT NUMBER: 99238449 PubMed ID: 10220385
TITLE: Three proteins define a class of human histone deacetylases related to yeast Hda1p.
AUTHOR: Grozinger C M; Hassig C A; Schreiber S L
CORPORATE SOURCE: Departments of Chemistry and Chemical Biology and Molecular and Cellular Biology, Harvard University, 12 Oxford Street, Cambridge, MA 02138, USA.
CONTRACT NUMBER: GM38627 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1999 Apr 27) 96 (9) 4868-73.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF132607; GENBANK-AF132608; GENBANK-AF132609
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990618

Last Updated on STN: 19990618
Entered Medline: 19990610

AB Gene expression is in part controlled by chromatin remodeling factors and the acetylation state of nucleosomal histones. The latter process is regulated by histone acetyltransferases and histone deacetylases (HDACs). Previously, three human and five yeast HDAC enzymes had been identified. These can be categorized into two classes: the first class represented by yeast Rpd3-like proteins and the second by yeast Hda1-like proteins. Human HDAC1, HDAC2, and HDAC3 proteins are members of the first class, whereas no class II human HDAC proteins had been identified. The amino acid sequence of Hda1p was used to search the GenBank/**expressed sequence tag databases** to identify partial sequences from three putative class II human HDAC proteins. The corresponding full-length cDNAs were cloned and defined as HDAC4, HDAC5, and HDAC6. These proteins possess certain features present in the conserved catalytic domains of class I human HDACs, but also contain additional sequence domains. Interestingly, HDAC6 contains an internal duplication of two catalytic domains, which appear to function independently of each other. These class II HDAC **proteins** have differential **mRNA expression** in human tissues and possess in vitro HDAC activity that is inhibited by trichostatin A. Coimmunoprecipitation experiments indicate that these HDAC proteins are not components of the previously identified HDAC1 and HDAC2 NRD and mSin3A complexes. However, HDAC4 and HDAC5 associate with HDAC3 in vivo. This finding suggests that the human class II HDAC enzymes may function in cellular processes distinct from those of HDAC1 and HDAC2.

L26 ANSWER 26 OF 35 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 22
ACCESSION NUMBER: 2000:63109 CAPLUS
DOCUMENT NUMBER: 132:74378
TITLE: A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
AUTHOR(S): Asamizu, Erika; Nakamura, Yasukazu; Sato, Shusei; Fukuzawa, Hideya; Tabata, Satoshi
CORPORATE SOURCE: Kazusa DNA Research Institute, Chiba, 292-0812, Japan
SOURCE: DNA Research (1999), 6(6), 369-373
CODEN: DARSE8; ISSN: 1340-2838
PUBLISHER: Universal Academy Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To understand genetic information carried in a unicellular green alga, Chlamydomonas reinhardtii, normalized and size-selected cDNA libraries were constructed from cells at photoautotrophic growth, and a total of 11,571 5'-end sequence tags were established. These sequences were grouped into 3433 independent EST species. Similarity search against the public non-redundant protein database indicated that 817 groups showed significant similarity to registered sequences, of which 140 were of previously identified C. reinhardtii genes, but the remaining 2616 species were novel sequences. The coverage of full-length protein coding regions was estd. to be over 60%. These cDNA clones and EST sequence information will provide a powerful source for the future genome-wide functional anal. of uncharacterized genes. Search results including the names of proteins encoded by the C. reinhardtii genes and other organisms and all the EST clones with their accession nos. are provided through the Internet at http://www.kazusa.or.jp/en/plant/chlamy/EST/. [This abstr. record is the

second of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L26 ANSWER 27 OF 35 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:444326 CAPLUS
DOCUMENT NUMBER: 131:98206
TITLE: Prostate cancer expression profiling by cDNA sequencing analysis
AUTHOR(S): Huang, Guyang Matthew; Ng, Wai-lap; Farkas, James; He, Lei; Liang, Hongyu Annie; Gordon, David; Yu, Jun; Hood, Leroy
CORPORATE SOURCE: Department of Molecular Biotechnology, University of Washington, Seattle, WA, 98195, USA
SOURCE: Genomics (1999), 59(2), 178-186
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Prostate cancer is a frequently diagnosed solid tumor that is originated mostly from prostate epithelium. One of the key issues in prostate cancer research is to develop mol. markers that can effectively detect and distinguish the progression and malignancy of prostate tumors. Automated, single-pass cDNA sequencing was utilized to rapidly identify expressed genes in a no. of cDNA libraries constructed from various normal and tumor prostatic tissues. These included cell lines as well as short-term epithelial culture. A total of 6604 expressed sequence tags (ESTs) were generated and searched against online nucleotide and protein databases. A relational database centric software system was constructed to process, store, and analyze EST data rapidly. cDNA contigs were also obtained by assembly of multiple EST sequences. Protein structural signatures were annotated using motif anal. tools including BLOCKS and an inhouse-designed neural network. Cross-library comparisons revealed their unique gene expression profiles. Several differentially expressed cDNA clones were identified, and their expression patterns were confirmed by RNA dot blot and RT-PCR analyses. (c) 1999 Academic Press.
REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 28 OF 35 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 1999307671 MEDLINE
DOCUMENT NUMBER: 99307671 PubMed ID: 10375612
TITLE: Identification of c-myc promoter-binding protein and X-box binding protein 1 as interleukin-6 target genes in human multiple myeloma cells.
AUTHOR: Wen X Y; Stewart A K; Sooknanan R R; Henderson G; Hawley T S; Reimold A M; Glimcher L H; Baumann H; Malek L T; Hawley R G
CORPORATE SOURCE: Oncology Research, University Health Network, Toronto, Ontario M5G 2M1, Canada.
CONTRACT NUMBER: CA26122 (NCI)
SOURCE: INTERNATIONAL JOURNAL OF ONCOLOGY, (1999 Jul) 15 (1) 173-8.

Journal code: 9306042. ISSN: 1019-6439.
PUB. COUNTRY: Greece
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199908
ENTRY DATE: Entered STN: 19990816
Last Updated on STN: 19990816
Entered Medline: 19990805

AB Interleukin-6 (IL-6) is implicated in the in vivo proliferation of malignant plasma cells in multiple myeloma. To define the molecular basis of the IL-6-induced mitogenic response in myeloma cells, we applied STAR (subtractive transcriptional amplification of **mRNA**), a new differential **expression** analysis technology, to isolate **mRNAs** preferentially **expressed** in IL-6-treated versus untreated cultures of the factor-responsive myeloma cell line U266. From the resulting collection of STAR clones, sequence information was obtained for a total of 72 distinct transcripts. Of these, 29 were found to correspond to known genes, 22 matched **expressed** sequence **tags** in public **databases** and 21 showed no sequence similarity to any existing entries. Among the known genes uncovered in the screen were those encoding proteins that function in cell division, cell signalling and gene/**protein expression**. Northern blot analysis documented that two transcription factor genes chosen for further study, c-myc promoter-binding protein (MBP-1) and X-box binding protein 1 (XBP-1), were up-regulated in U266 cells about 3-fold relative to the cell cycle-dependent beta-actin gene 12 h after IL-6 treatment. Both genes were also similarly up-regulated by IL-6 in factor-dependent ANBL-6 myeloma cells. These results indicate that MBP-1 and XBP-1 are IL-6 genes in myeloma cells; as such, they may play a role in IL-6-mediated growth control in multiple myeloma.

L26 ANSWER 29 OF 35 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:711831 CAPLUS
DOCUMENT NUMBER: 130:105868
TITLE: Gene discovery in the wood-forming tissues of poplar: analysis of 5,692 expressed sequence tags
AUTHOR(S): Sterky, Fredrik; Regan, Sharon; Karlsson, Jan; Hertzberg, Magnus; Rohde, Antje; Holmberg, Anders; Amini, Bahram; Bhalerao, Rupali; Larsson, Magnus; Villarroel, Raimundo; Van Montagu, Marc; Sandberg, Goran; Olsson, Olof; Teeri, Tuula T.; Boerjan, Wout; Gustafsson, Petter; Uhlen, Mathias; Sundberg, Bjorn; Lundeberg, Joakim
CORPORATE SOURCE: Department of Biotechnology, Kungl Tekniska Hogskolan, Royal Institute of Technology, Stockholm, SE-10044, Swed.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1998), 95(22), 13330-13335
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A rapidly growing area of genome research is the generation of expressed

sequence tags (ESTs) in which large nos. of randomly selected cDNA clones are partially sequenced. The collection of ESTs reflects the level and complexity of gene expression in the sampled tissue. To date, the majority of plant ESTs are from nonwoody plants such as Arabidopsis, Brassica, maize, and rice. Here, we present a large-scale prodn. of ESTs from the wood-forming tissues of two poplars, Populus tremula L. .times. tremuloides Michx. and Populus trichocarpa "Trichobel". The 5,692 ESTs analyzed represented a total of 3,719 unique transcripts for the two cDNA libraries. Putative functions could be assigned to 2,245 of these transcripts that corresponded to 820 protein functions. Of specific interest to forest biotechnol. are the 4% of ESTs involved in various processes of cell wall formation, such as lignin and cellulose synthesis, 5% similar to developmental regulators and members of known signal transduction pathways, and 2% involved in hormone biosynthesis. An addnl. 12% of the ESTs showed no significant similarity to any other DNA or protein sequences in existing databases. The absence of these sequences from public databases may indicate a specific role for these proteins in wood formation. The cDNA libraries and the accompanying database are valuable resources for forest research directed toward understanding the genetic control of wood formation and future endeavors to modify wood and fiber properties for industrial use.

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 30 OF 35 MEDLINE DUPLICATE 24

ACCESSION NUMBER: 1998187249 MEDLINE
DOCUMENT NUMBER: 98187249 PubMed ID: 9526501
TITLE: NAD(+)-dependent isocitrate dehydrogenase from Arabidopsis thaliana. Characterization of two closely related subunits.
AUTHOR: Behal R H; Oliver D J
CORPORATE SOURCE: Department of Botany, Iowa State University, Ames 50011-1020, USA.
SOURCE: PLANT MOLECULAR BIOLOGY, (1998 Mar) 36 (5) 691-8. Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF015923; GENBANK-U81993; GENBANK-U81994; GENBANK-U82203
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980430
Last Updated on STN: 20000303
Entered Medline: 19980421

AB Two cDNA clones which appear to encode different subunits of NAD(+)-dependent isocitrate dehydrogenase (IDH; EC 1.1.1.41) were identified by homology searches from the Arabidopsis **EST database**. These cDNA clones were obtained and sequenced; both encoded full-length messages and displayed 82.7% nucleotide sequence identity over the coding region. The deduced amino acid sequences revealed preprotein lengths of 367 residues, with an amino acid identity of 86.1%. Genomic Southern blot analysis showed distinct single-copy genes for both IDH subunits. Both IDH subunits were **expressed** as recombinant **proteins** in Escherichia coli, and polyclonal antibodies were raised to each subunit. The Arabidopsis **cDNA** clones were **expressed** in Saccharomyces cerevisiae mutants which were deficient

in either one or both of the yeast NAD(+)-dependent IDH subunits. The Arabidopsis cDNA clones failed to complement the yeast mutations; although both IDH-I and IDH-II were expressed at detectable levels, neither protein was imported into the mitochondria.

L26 ANSWER 31 OF 35 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 97376836 MEDLINE
DOCUMENT NUMBER: 97376836 PubMed ID: 9233607
TITLE: A novel human CC chemokine PARC that is most homologous to macrophage-inflammatory protein-1 alpha/LD78 alpha and chemotactic for T lymphocytes, but not for monocytes.
AUTHOR: Hieshima K; Imai T; Baba M; Shoudai K; Ishizuka K; Nakagawa T; Tsuruta J; Takeya M; Sakaki Y; Takatsuki K; Miura R; Opdenakker G; Van Damme J; Yoshie O; Nomiyama H
CORPORATE SOURCE: Department of Biochemistry, Kumamoto University Medical School, Japan.
SOURCE: JOURNAL OF IMMUNOLOGY, (1997 Aug 1) 159 (3) 1140-9. Journal code: 2985117R. ISSN: 0022-1767.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
OTHER SOURCE: GENBANK-AB000221
ENTRY MONTH: 199708
ENTRY DATE: Entered STN: 19970825
Last Updated on STN: 19970825
Entered Medline: 19970814

AB By searching the **expressed** sequence **tag** (**EST**) **database**, we identified partial cDNA sequences encoding a polypeptide with significant sequence identity to the human CC chemokine macrophage-inflammatory protein-1 alpha (MIP-1 alpha)/LD78 alpha. We determined the complete cDNA sequence that contained a reading frame of 89 amino acids with 61% identity to human MIP-1 alpha/LD78 alpha. The **mRNA** was **expressed** constitutively at high levels in human lung and at low levels in some lymphoid tissues. Furthermore, the mRNA was strongly induced in several human cell lines, including monocytic U937 cells, by PMA. From these results, we designated this novel CC chemokine as PARC from pulmonary and activation-regulated chemokine. In situ hybridization analyses showed that alveolar macrophages, follicular dendritic cells in the germinal centers of regional lymph nodes, and peripheral blood monocytes stimulated with LPS **express** PARC **mRNA**. Using the human CC chemokine yeast artificial chromosome contig that we constructed recently, we mapped the PARC gene (SCYA18) within one of the two subregions of the CC chemokine gene cluster at chromosome 17q11.2. To investigate its biologic activity, the PARC **protein** was **expressed** in insect cells. PARC was chemotactic for both activated (CD3+) T cells and nonactivated (CD14-) lymphocytes, but not for monocytes or granulocytes. Binding analysis using PARC fused with alkaline phosphatase-(His)6 showed the presence of a single class of receptors for PARC on lymphocytes with a Kd of 1.9 nM and 590 sites/cell. Thus, PARC is a novel CC chemokine with a close phylogenic relationship with MIP-1 alpha/LD78 alpha, but with a highly selective activity on lymphocytes.

L26 ANSWER 32 OF 35 MEDLINE DUPLICATE 26
ACCESSION NUMBER: 1998030400 MEDLINE
DOCUMENT NUMBER: 98030400 PubMed ID: 9365118
TITLE: Novel lymphocyte-specific CC chemokines and their receptors.
AUTHOR: Yoshie O; Imai T; Nomiyama H
CORPORATE SOURCE: Shionogi Institute for Medical Science, Osaka, Japan.
SOURCE: JOURNAL OF LEUKOCYTE BIOLOGY, (1997 Nov) 62 (5) 634-44.
Ref: 47
Journal code: 8405628. ISSN: 0741-5400.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109
Entered Medline: 19971208

AB By using a cloning method termed the signal sequence trap as well as by searching for chemokine homologous sequences in the **database** of **expressed** sequence **tags**, **cDNA** fragments potentially encoding novel CC chemokines were initially identified. Using these sequences, we have cloned five novel human CC chemokines termed TARC, LARC, ELC, SLC, and PARC. These chemokines are constitutively expressed especially in some lymphoid tissues with individually unique **expression** patterns. The recombinant **proteins** are all found to be selectively chemotactic for lymphocytes but not for monocytes or neutrophils. Each chemokine appears to interact with a class of receptors on lymphocytes that is not shared by any other chemokines so far tested. Furthermore, we have identified CCR4 as the specific receptor for TARC, GPR-CY4/DRY6/CKR-L3/STRL22 as that for LARC (CCR6), and EBI1/BLR2 as that for ELC (CCR7). Only the gene for PARC is mapped to the traditional CC chemokine gene cluster at chromosome 17q11.2, whereas those for TARC, LARC, ELC, and SLC are localized at different loci. Collectively, these five CC chemokines may constitute a new category of CC chemokines that are involved in trafficking and homing of particular subsets of lymphocytes in particular lymphoid tissue microenvironments.

L26 ANSWER 33 OF 35 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 97245716 MEDLINE
DOCUMENT NUMBER: 97245716 PubMed ID: 9090384
TITLE: Isolation of the human PEX12 gene, mutated in group 3 of the peroxisome biogenesis disorders.
AUTHOR: Chang C C; Lee W H; Moser H; Valle D; Gould S J
CORPORATE SOURCE: Department of Biological Chemistry, Johns Hopkins University School of Medicine, Baltimore, Maryland 21205-2185, USA.
CONTRACT NUMBER: DK45787 (NIDDK)
HD10981 (NICHD)
SOURCE: NATURE GENETICS, (1997 Apr) 15 (4) 385-8.
Journal code: 9216904. ISSN: 1061-4036.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-U58140; GENBANK-U91521; GENBANK-U91522; GENBANK-Z49211; GENBANK-Z68104
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970507
Last Updated on STN: 19970507
Entered Medline: 19970425

AB The peroxisome biogenesis disorders (PBDs) are a group of genetically heterogeneous diseases lethal in early infancy. Although the clinical features of PBD patients may vary, cells from all PBD patients exhibit a defect in the import of one or more classes of peroxisomal matrix proteins. This cellular phenotype is shared by yeast pex mutants, and human orthologues of yeast PEX genes have been shown to be defective in some groups of PBD patients. We identified a putative human orthologue of ScPEX12 by screening the **database** of **expressed** sequence **tags** for **cDNAs** capable of encoding a protein similar to yeast Pex12p. Although its sequence similarity to yeast Pex12 proteins was limited, PEX12 shared the same subcellular distribution as yeast Pex12p and localized to the peroxisome membrane. PEX12 **expression** restored peroxisomal **protein** import in fibroblasts from PBD patients of complement group 3 (CG3) and frameshift mutations in PEX12 were detected in two unrelated CG3 patients. These data demonstrate that mutations in PEX12 are responsible for CG3 of the PBD and that PEX12 plays an essential role in peroxisomal matrix protein import.

L26 ANSWER 34 OF 35 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:506100 CAPLUS
DOCUMENT NUMBER: 127:215778
TITLE: A survey of genes expressed in mouse embryonal carcinoma F9 cells: characterization of expressed sequence tags matching no known genes
AUTHOR(S): Nomura, Midori; Nishiguchi, Seiji; Motaleb, Md. Abdul; Takihara, Yoshihiro; Takagi, Tatsuya; Yasunaga, Teruo; Shimada, Kazunori
CORPORATE SOURCE: Department of Medical Genetics, Division of Molecular Biomedicine, Research Institute for Microbial Diseases, Osaka University, Osaka, 565, Japan
SOURCE: Journal of Biochemistry (Tokyo) (1997), 122(1), 129-147
CODEN: JOBIAO; ISSN: 0021-924X
PUBLISHER: Japanese Biochemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We prepd. 2,132 expressed sequence tags (ESTs) from undifferentiated mouse embryonal carcinoma F9 cells and found that 1,416 match known gene and/or protein sequences. To obtain information on the functions of the remaining 716 unidentified ESTs and to develop a system for characterizing ESTs matching no known genes, we analyzed their sequences by (i) repeated database searches, using the BLASTN, BLASTX, TBLASTX, and FASTA programs, (ii) using computer programs developed or modified for this work, such as the WFASTA, ORFTRNS, and MFASTA programs, together with the DBPROSITE and GRAIL programs, and (iii) examg. the expression patterns of the corresponding mRNAs in F9 cells and several organs of adult mice, using the digoxigenin-labeled dot-blot method. We found that 216 of the 716 ESTs match known gene and/or protein sequences, and 307 show significant similarities to these sequences, with a Poisson p-value < 0.01. The

strategy and usefulness of such anal. for characterizing unidentified ESTs
are discussed.

L26 ANSWER 35 OF 35 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 94324994 MEDLINE
DOCUMENT NUMBER: 94324994 PubMed ID: 8048971
TITLE: Cataloging of the genes expressed in human keratinocytes: analysis of 607 randomly isolated cDNA sequences.
AUTHOR: Konishi K; Morishima Y; Ueda E; Kibe Y; Nonomura K; Yamanishi K; Yasuno H
CORPORATE SOURCE: Department of Dermatology, Kyoto Prefectural University of Medicine, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1994 Jul 29) 202 (2) 976-83.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D29018; GENBANK-D29019; GENBANK-D29020; GENBANK-D29021; GENBANK-D29022; GENBANK-D29023; GENBANK-D29024; GENBANK-D29025; GENBANK-D29026; GENBANK-D29027; GENBANK-D29028; GENBANK-D29029; GENBANK-D29030; GENBANK-D29031; GENBANK-D29032; GENBANK-D29033; GENBANK-D29034; GENBANK-D29035; GENBANK-D29036; GENBANK-D29037; GENBANK-D29038; GENBANK-D29039; GENBANK-D29040; GENBANK-D29041; GENBANK-D29042; GENBANK-D29043; GENBANK-D29044; GENBANK-D29045; GENBANK-D29046; GENBANK-D29047
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19940909
Last Updated on STN: 19960129
Entered Medline: 19940901

AB The partial nucleotide sequences of 607 cDNAs randomly isolated from a cDNA library of cultured human epidermal keratinocytes were determined by single pass sequencing. Homology search of the sequences to the non-redundant nucleotide **databases** revealed that 27% of the cDNAs matched registered human-or non-human genes encoding not only keratinocyte specific genes, but also a variety of functional **proteins**, the **expression** of which had not been identified in keratinocytes. Non-matching cDNAs covering 49% of the cDNAs were not homologous even to **ESTs** from other organs, suggesting that these **cDNAs** include novel genes **expressed** in the cells. The large scale sequencing of keratinocyte cDNAs provides a useful molecular source for research into biology and diseases of the skin.

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=> s ("in"(w)silico) and (virtual(2a)northern)
L27          0 ("IN"(W) SILICO) AND (VIRTUAL(2A) NORTHERN)

=> s ("in"(w)silico) or (virtual(2a)northern)
L28        146 ("IN"(W) SILICO) OR (VIRTUAL(2A) NORTHERN)

=> s l28 and (express?(2a)pattern#)
L29          8 L28 AND (EXPRESS?(2A) PATTERN#)

=> dup rem l29
PROCESSING COMPLETED FOR L29
L30          8 DUP REM L29 (0 DUPLICATES REMOVED)
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=> d ibib abs tot

L30 ANSWER 1 OF 8 MEDLINE
ACCESSION NUMBER: 2001486784 MEDLINE
DOCUMENT NUMBER: 21385003 PubMed ID: 11493597
TITLE: **In silico** identification of novel selenoproteins in the Drosophila melanogaster genome.
AUTHOR: Castellano S; Morozova N; Morey M; Berry M J; Serras F; Corominas M; Guigo R
CORPORATE SOURCE: Grup de Recerca en Informatica Biomedica, Institut Municipal d'Investigacio Medica, Universitat Pompeu Fabra, Dr. Aiguader 80, 08003 Barcelona, Spain.
SOURCE: EMBO Rep, (2001 Aug) 2 (8) 697-702.
Journal code: 100963049. ISSN: 1469-221X.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20020121
Entered Medline: 20011212

AB In selenoproteins, incorporation of the amino acid selenocysteine is specified by the UGA codon, usually a stop signal. The alternative decoding of UGA is conferred by an mRNA structure, the SECIS element, located in the 3'-untranslated region of the selenoprotein mRNA. Because of the non-standard use of the UGA codon, current computational gene prediction methods are unable to identify selenoproteins in the sequence of the eukaryotic genomes. Here we describe a method to predict selenoproteins in genomic sequences, which relies on the prediction of SECIS elements in coordination with the prediction of genes in which the strong codon bias characteristic of protein coding regions extends beyond a TGA codon interrupting the open reading frame. We applied the method to the Drosophila melanogaster genome, and predicted four potential selenoprotein genes. One of them belongs to a known family of selenoproteins, and we have tested experimentally two other predictions with positive results. Finally, we have characterized the **expression pattern** of these two novel selenoprotein genes.

L30 ANSWER 2 OF 8 MEDLINE
ACCESSION NUMBER: 2001654579 MEDLINE
DOCUMENT NUMBER: 21564115 PubMed ID: 11707285
TITLE: **In silico** screening for tumour-specific expressed sequences in human genome.
AUTHOR: Baranova A V; Lobashev A V; Ivanov D V; Krukovskaya L L; Yankovsky N K; Kozlov A P
CORPORATE SOURCE: Vavilov Institute of General Genetics, 3 Gubkina Str., Moscow 119991, Russia.. baranova@vigg.ru
SOURCE: FEBS LETTERS, (2001 Nov 9) 508 (1) 143-8.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011115
Last Updated on STN: 20020123
Entered Medline: 20011214

AB A computer-based differential display tool named HsAnalyst has been developed and successfully used for the comparison of **expression**

patterns in a set of tumours versus a set of normal tissues. A list of EST clusters highly represented in tumours and rarely observed in normal tissues has been developed as a resulting output file of the program. These differentially expressed EST clusters (genes) can be useful for developing new tumour markers and prognostic indicators for a wide set of human malignancies. Tumour-specific protein-coding genes may be considered a manifestation of tumour-specific gene expression.

L30 ANSWER 3 OF 8 MEDLINE
ACCESSION NUMBER: 2000410547 MEDLINE
DOCUMENT NUMBER: 20360649 PubMed ID: 10902192
TITLE: **In silico** analysis of gene **expression patterns** during early development of Xenopus laevis.
AUTHOR: Pollet N; Schmidt H A; Gawantka V; Niehrs C; Vingron M
CORPORATE SOURCE: Department of Theoretical Bioinformatics, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld, Germany.
SOURCE: PACIFIC SYMPOSIUM ON BIOCOMPUTING, (2000) 443-54. Journal code: 9711271.
PUB. COUNTRY: Singapore
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000829

AB The information as to where and when a mRNA is present in a given cell is essential to bridge the gap between the DNA sequence of a gene and its physiological function. Therefore, a major component of functional genomics is to characterize the levels and the spatio-temporal domains of gene expression. Currently, there is just a few specialised public databases available storing the data on gene expression while they are needed as a resource for the field. Moreover, there is a need to develop and assess computational tools to compare and analyse expression profiles in a suitable way for biological interpretation. Here we describe our recent work on developing a database on gene expression for the frog Xenopus laevis, and on setting up and using new tools for the analysis and comparison of gene **expression patterns**. We used histogram clustering to compare expression profiles at both gene and tissue levels using a set of data coming from the characterization of the expression of genes during early development of Xenopus. This enabled us to draw a tree of tissue relatedness and to identify coexpressed genes by in silico analysis.

L30 ANSWER 4 OF 8 MEDLINE
ACCESSION NUMBER: 2000195631 MEDLINE
DOCUMENT NUMBER: 20195631 PubMed ID: 10729227
TITLE: Characterization of a novel gene, C21orf6, mapping to a critical region of chromosome 21q22.1 involved in the monosomy 21 phenotype and of its murine ortholog, orf5.
AUTHOR: Orti R; Rachidi M; Vialard F; Toyama K; Lopes C; Taudien S; Rosenthal A; Yaspo M L; Sinet P M; Delabar J M
CORPORATE SOURCE: UMR 8602 CNRS, UFR Necker Enfants-Malades, 156 rue de Vaugirard, Paris, 75730, France.
SOURCE: GENOMICS, (2000 Mar 1) 64 (2) 203-10. Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF177771; GENBANK-Y19009
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000518
Last Updated on STN: 20000518
Entered Medline: 20000511

AB Phenotypic and molecular analyses of patients with partial chromosome 21 monosomy enabled us to define a region, spanning 2.4 Mb between D21S190 and D21S226, associated with arthrogryposis, mental retardation, hypertonia, and several facial anomalies. The markers of the region were used to screen a total human PAC library (Ioannou, RZPD). We isolated 57 PACs, which formed primary contigs. EST clusters (UNIGENE collection) located in a 6-Mb interval, between D21S260 and D21S263, were mapped in individual bacterial clones. We mapped the WI-17843 cluster to the PAC clone J12100, which contains the two anchor markers LB10T and LA329. The open reading frame extends over 960 bp, with three putative start codons. The 1695-bp cDNA containing a polyadenylation signal should correspond to the full-length cDNA. From the genomic sequence, we deduced that the gene contained five exons and that there was a putative promoter sequence upstream from exon 1. **In silico** screening of DNA databases revealed similarity with a murine EST. The corresponding cDNA (1757 bp) sequence was very similar (>85%) to the human cDNA and had an open reading frame of 876 nucleotides. Somatic hybrid mapping localized the cDNA to mouse chromosome 16. EST analyses and RT-PCR indicated that the third exon in the human gene (exon 2 in the mouse) undergoes alternative splicing. Northern blot hybridization showed that the gene was ubiquitously expressed in humans and mice. The longest mouse clone was used to generate riboprobes, which were hybridized to murine embryos at stages E-9.5, E-10.5, E-12.5, E-13.5, and E-14.5-15, to study the **pattern** of **expression** during development. Ubiquitous labeling was observed, with strong signals restricted to limited areas of the telencephalon, the mesencephalon, and the interrhombomeric regions in the central nervous system, and other regions of the body such as the limb buds, branchial arches, and somites.

L30 ANSWER 5 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:135027 BIOSIS
DOCUMENT NUMBER: PREV200100135027
TITLE: Gene expression profiling in acute spinal cord injury: effects of methylprednisolone.
AUTHOR(S): Hart, R. P. (1); Ji, Y.; Liu, J.; Huang, W.; Young, W.
CORPORATE SOURCE: (1) Rutgers Univ, Newark, NJ USA
SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-864.13. print.
Meeting Info.: 30th Annual Meeting of the Society of Neuroscience New Orleans, LA, USA November 04-09, 2000 Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Acute contusion injury of spinal cord results in a complex program of gene regulation including inflammation, stress response, wound repair and regrowth. We have used gene arrays to determine patterns of gene responses

associated with injury and pharmacological intervention. Initial experiments examined the effect of the standard methylprednisolone (MP) treatment on acute injury. Rats were contused using the MASCIS impactor, then injected with 30 mg/kg MP or saline. Two hours following injury, segments of spinal cord were removed from the site of injury and used to prepare poly(A)+ RNA. Probe cDNA was hybridized in triplicate with Clontech Atlas 1.2 macroarrays containing 1,176 known gene probes. Results indicate that only 20 genes are significantly regulated by injury over control ($p < 0.05$ by Student's t test), and that 38 genes are significantly different when comparing injured saline infusion to MP treatment. Clustering analysis indicates that MP increases relative expression of several metabolic functions, and decreases several signaling genes, including NPY and TRH. To identify all genes that are regulated following acute spinal cord injury, we have begun a subtractive hybridization screen. cDNA was prepared from rats injured for 0-24 hrs and subtracted using the Clontech PCR-Select kit. Regulation was confirmed using **virtual Northern** blots. Few genes appear to be increased after acute injury, but a large group was found to be reduced. Identification of gene **expression patterns** following spinal cord injury provide new insight into injury responses and aid in identifying new therapies.

L30 ANSWER 6 OF 8 MEDLINE
ACCESSION NUMBER: 1999400797 MEDLINE
DOCUMENT NUMBER: 99400797 PubMed ID: 10471358
TITLE: Chromosomal, in silico and in vitro expression analysis of cardiovascular-based genes encoding zinc finger proteins.
AUTHOR: Dai K S; Liew C C
CORPORATE SOURCE: The Cardiac Gene Unit, Institute of Medical Science Department of Laboratory Medicine and Pathobiology, University of Toronto, Ontario, Canada.
SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1999 Sep) 31 (9) 1749-69.
Journal code: 0262322. ISSN: 0022-2828.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991014
Last Updated on STN: 19991014
Entered Medline: 19991004

AB Three hundred and sixty expressed sequence tags (ESTs) from human heart cDNA libraries corresponding to one hundred and twenty six unique zinc finger proteins (ZFPs) were annotated and classified into seven types of ZFPs as reported previously. Among these 126 cvbZFPs (cardiovascular-based ZFPs), the C(2)H(2)-type and the C(2)C(2)-type are the two major ZFP types which account for more than 80% of ZFP genes present in the cardiovascular system. The **expression patterns** of 11 randomly selected ZFP genes (at least one for each type) in normal fetal, adult and hypertrophic adult hearts, respectively, were determined using reverse transcriptase-polymerase chain reaction (RT-PCR) analysis. The results suggest that ZFPs may be involved in the processes of either developmental

control (downregulated or upregulated expression) or basic cellular functional regulation (constant expression). Interestingly, PAF-1 (peroxisome assembly factor-1), a C(3)HC(4)-type ZFP (RING domain-containing ZFP) showing a downregulated **expression pattern** in normal tissues was found to be upregulated in hypertrophic adult heart, suggesting a possible role for this fetal gene in the pathogenesis of cardiac hypertrophy. **In silico** Northern analysis of 15 tissues showed that over 90% of cvbZFPs demonstrate widespread tissue distribution, suggesting the vast majority of ZFPs are functionally shared among tissues. The potential importance of transcriptional repressors in cardiovascular development and disease, such as HFHZ, was supported by the observation that one-third (39 of 126) of cvbZFPs possess this function. Of these, 26 are C(2)H(2)-type and the remaining 13 included 8 C(2)C(2)-type, 1 C(3)HC(4)-type, 1 C(2)HC(4)C(HD)-type, 2 C(3)H-type and 1 combination type. Of particular interest was the observation that ZFPs which contain a KRAB domain are the major subtype present (51. 3% of the total repressors in cvbZFPs). Chromosomal distribution analysis showed that mapping loci of cvbZFP genes are concentrated on chromosomes 1, 3, 6, 8, 10, 11, 12, 19 and X. In particular, chromosome 19 appears to be enriched in ZFP genes with C(2)H(2)-type as the predominant type present. Overall, this report provides a fundamental initial step toward understanding the potential role of ZFPs in regulating cadiac development and disease.

L30 ANSWER 7 OF 8 MEDLINE
ACCESSION NUMBER: 1999013437 MEDLINE
DOCUMENT NUMBER: 99013437 PubMed ID: 9799093
TITLE: **In silico**-initiated cloning and molecular characterization of a novel human member of the L1 gene family of neural cell adhesion molecules.
AUTHOR: Wei M H; Karavanova I; Ivanov S V; Popescu N C; Keck C L; Pack S; Eisen J A; Lerman M I
CORPORATE SOURCE: Intramural Research Support Program, SAIC Frederick, National Cancer Institute-Frederick Cancer Research and Development Center, MD 21702-1201, USA.
CONTRACT NUMBER: NO1-CO-56000 (NCI)
SOURCE: HUMAN GENETICS, (1998 Sep) 103 (3) 355-64. Journal code: 7613873. ISSN: 0340-6717.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981119

AB To discover genes contributing to mental retardation in 3p- syndrome patients we have used in silico searches for neural genes in NCBI databases (dbEST and Uni-Gene). An EST with strong homology to the rat CAM L1 gene subsequently mapped to 3p26 was used to isolate a full-length cDNA. Molecular analysis of this cDNA, referred to as CALL (cell adhesion L1-like), showed that it is encoded by a chromosome 3p26 locus and is a novel member of the L1 gene family of neural cell adhesion molecules. Multiple lines of evidence suggest CALL is likely the human ortholog of the murine gene CHL1: it is 84% identical on the protein level, has the

same domain structure, same membrane topology, and a similar **expression pattern**. The orthology of CALL and CHL1 was confirmed by phylogenetic analysis. By in situ hybridization, CALL is shown to be expressed regionally in a timely fashion in the central nervous system, spinal cord, and peripheral nervous system during rat development. Northern analysis and EST representation reveal that it is expressed in the brain and also outside the nervous system in some adult human tissues and tumor cell lines. The cytoplasmic domain of CALL is conserved among other members of the L1 subfamily and features sequence motifs that may involve CALL in signal transduction pathways.

L30 ANSWER 8 OF 8 MEDLINE
ACCESSION NUMBER: 1998086396 MEDLINE
DOCUMENT NUMBER: 98086396 PubMed ID: 9425316
TITLE: Identification and primary structure of five human NADH-ubiquinone oxidoreductase subunits.
AUTHOR: Ton C; Hwang D M; Dempsey A A; Liew C C
CORPORATE SOURCE: Department of Laboratory Medicine & Pathobiology, University of Toronto, Toronto Hospital, Ontario, Canada.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997 Dec 18) 241 (2) 589-94.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF047181; GENBANK-AF047182; GENBANK-AF047183; GENBANK-AF047184; GENBANK-AF047185
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980206
Last Updated on STN: 20000303
Entered Medline: 19980126

AB The multi-subunit NADH-ubiquinone oxidoreductase (complex I) is the first enzyme complex in the electron transport chain of mitochondria. A small number of NADH-ubiquinone oxidoreductase subunits are the products of mitochondrial genes (subunits 1-7), while the remainder are nuclear encoded and imported from the cytoplasm. We have isolated and sequenced five subunits of the human complex I from a human heart lambda ZAP Express cDNA library. Comparison of the deduced amino acid sequences of the human subunits with the corresponding bovine sequences revealed greater than 80% amino acid identity. The high degree of similarity between human and bovine sequences suggests functional conservation of these subunits in the complex I. **In silico** Northern analysis revealed that two of the subunits were expressed ubiquitously while the remainder may have more restricted **patterns** of **expression**.

=> d history

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L4 42 S ORTHOLOG AND PY<1995
L5 27 S ORTHOLOG AND PY<1994
L6 21 S ORTHOLOG AND PY<1993

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L7           15 S ORTHOLOG AND PY<1992

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     15:19:03 ON 09 JUL 2002
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L10          26 S L8 AND (RAS(W)LIKE)
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L13        4464 S BEASLEY?/AU
L14        6870 S L11 OR L12 OR L13
L15           0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
L16          10 DUP REM L10 (16 DUPLICATES REMOVED)
L17         164 S L8 AND (VIRTUAL)
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L19           0 S L14 AND (VIRTUAL(3A)NORTHERN)
L20      266508 S (MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#)(3A)EXPRESS?
L21      336550 S (PROTEIN# OR PEPTIDE# OR TRANSLAT?)(3A)EXPRESS?
L22       37711 S L20(S)L21
L23      183803 S EST OR ESTS OR (EXPRESSED(3W)TAG#)
L24         286 S L22(S)L23
L25         100 S L24(S)DATABASE#
L26          35 DUP REM L25 (65 DUPLICATES REMOVED)
L27           0 S ("IN"(W)SILICO) AND (VIRTUAL(2A)NORTHERN)
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L29           8 S L28 AND (EXPRESS?(2A)PATTERN#)
L30           8 DUP REM L29 (0 DUPLICATES REMOVED)

=> s l28 and ("not" or cannot)
L31           1 L28 AND ("NOT" OR CANNOT)

=> d ibib abs tot

L31  ANSWER 1 OF 1  BIOSIS  COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER:   2001:487312  BIOSIS
DOCUMENT NUMBER:    PREV200100487312
TITLE:              Subtractive cDNA analysis of spinal cord gene expression
                    following partial sciatic nerve injury (PSNL.
AUTHOR(S):          Coyle, D. E. (1)
CORPORATE SOURCE:   (1) Department of Anesthesia, Univ Cincinnati, Cincinnati,
                    OH USA
SOURCE:             Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1,
                    pp. 142. print.
                    Meeting Info.: 31st Annual Meeting of the Society for
                    Neuroscience San Diego, California, USA November 10-15,
                    2001
                    ISSN: 0190-5295.
DOCUMENT TYPE:      Conference
LANGUAGE:           English
SUMMARY LANGUAGE:   English
AB   Chronic allodynia develops slowly (days to weeks) following peripheral
     nerve injury and cannot be satisfactory explained without taking
     into account central mechanisms. This suggests that chronic allodynia
     requires a cascade of posttranslational and transcriptional events to
     occur before its development. In order to understand the molecular basis
     for the development of chronic allodynia this study has used the
     subtractive cDNA cloning method to isolate genes that are differentially
     expressed in the spinal cord following partial sciatic nerve ligation
     (PSNL). Three "full length" cDNA libraries were generated (normal female,
     PSNL 7-14, and 15-21 days post-injury). The normal female spinal cord
cDNA
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library (driver) was subtracted from both PSNL spinal cord cDNA libraries (target) by the method of Lin and Sargan (NeuroReport 6, 1981-1984 (1995)). The remaining clones that contained inserts were further screened by hybridization with Cy5-labeled cDNA probes generated from the driver cDNA library (fluorescent Southern Analysis). Of the clones that did not hybridize, the 25% displaying the lowest fluorescent intensity were sequenced (UC DNA Core Facility) and nucleic acid homology searches were performed using the BLAST program. Thirty-six distinct clones were identified and isolated of which 20 (56%) were known genes, 5 (14%) were unknown genes with EST matches, and 11 (30%) were novel genes. All genes were verified using RT-PCR using primers based on cDNA sequences and/or by **virtual northern** analysis. The identified clones indicate that both neurons and glia are involved in the process of change within the spinal cord following PSNL.

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=> d history

     (FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002)

     FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002
L1           168 S ORTHOLOG AND PY<1998
L2           106 S ORTHOLOG AND PY<1997
L3            65 S ORTHOLOG AND PY<1996
L4            42 S ORTHOLOG AND PY<1995
L5            27 S ORTHOLOG AND PY<1994
L6            21 S ORTHOLOG AND PY<1993
L7            15 S ORTHOLOG AND PY<1992

     FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT
     15:19:03 ON 09 JUL 2002
L8        350284 S YAN?/AU
L9             0 S L8 AND NADRIN#
L10           26 S L8 AND (RAS(W)LIKE)
L11         1054 S KETCHUM?/AU
L12         1550 S (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13         4464 S BEASLEY?/AU
L14         6870 S L11 OR L12 OR L13
L15            0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
L16           10 DUP REM L10 (16 DUPLICATES REMOVED)
L17          164 S L8 AND (VIRTUAL)
L18            0 S L8 AND (VIRTUAL(3A)NORTHERN)
L19            0 S L14 AND (VIRTUAL(3A)NORTHERN)
L20       266508 S (MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#)(3A)EXPRESS?
L21       336550 S (PROTEIN# OR PEPTIDE# OR TRANSLAT?)(3A)EXPRESS?
L22        37711 S L20(S)L21
L23       183803 S EST OR ESTS OR (EXPRESSED(3W)TAG#)
L24          286 S L22(S)L23
L25          100 S L24(S)DATABASE#
L26           35 DUP REM L25 (65 DUPLICATES REMOVED)
L27            0 S ("IN"(W)SILICO) AND (VIRTUAL(2A)NORTHERN)
L28          146 S ("IN"(W)SILICO) OR (VIRTUAL(2A)NORTHERN)
L29            8 S L28 AND (EXPRESS?(2A)PATTERN#)
L30            8 DUP REM L29 (0 DUPLICATES REMOVED)
L31            1 S L28 AND ("NOT" OR CANNOT)

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L32        84350 (EXPRESSION(2A) PATTERN#)
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PROCESSING COMPLETED FOR L33
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L34 ANSWER 1 OF 9 MEDLINE DUPLICATE 1

ACCESSION NUMBER: 2001637600 MEDLINE
DOCUMENT NUMBER: 21538920 PubMed ID: 11682602
TITLE: Hair follicle predetermination.
AUTHOR: Panteleyev A A; Jahoda C A; Christiano A M
CORPORATE SOURCE: Department of Dermatology, Columbia University, College of Physicians and Surgeons, 630 W. 168th Street, Vanderbilt Clinic VC-1526, New York, NY 10032, USA..
ap374@columbia.edu
CONTRACT NUMBER: P30-44534
RO1-47338
SOURCE: JOURNAL OF CELL SCIENCE, (2001 Oct) 114 (Pt 19) 3419-31.
Ref: 104
Journal code: 0052457. ISSN: 0021-9533.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011107
Last Updated on STN: 20020124
Entered Medline: 20011231

AB Recent genetic and molecular studies of hair follicle (HF) biology have provided substantial insight; however, the molecular data, including **expression patterns**, **cannot** be properly appreciated without an understanding of the basic cellular rearrangements and interactions that underpin HF cyclic transformations. We present a novel interpretation of the major cellular processes that take place during HF cycling--the hypothesis of hair follicle predetermination. This hypothesis is an extension of previous models of HF cellular kinetics but has two critical modifications: the dual origin of the cycling portion of the HF, and the timing of the recruitment of stem cells. A compilation of evidence suggests that the ascending portion of the HF (hair shaft and inner root sheath) arises not from bulge-located HF stem cells that contribute to the formation of only the outer root sheath (ORS), but instead from the germinative cells localized in the secondary hair germ. In middle anagen, upon completion of the downward growth of the HF, cells derived from the bulge region migrate downward along the ORS to reside at the periphery of the HF bulb as a distinct, inactive cell population that has specific patterns of gene expression - 'the lateral disc'. These cells survive catagen-associated apoptosis and, under the direct influence of the follicular papilla (FP), transform into the hair germ and acquire the ability to respond to FP signaling and produce a new hair. Thus, we propose that the specific sensitivity of germ cells to FP signaling and their commitment to produce the ascending HF layers are predetermined by the previous hair cycle during the process of transformation of bulge-derived lateral disc cells into the secondary hair germ.

L34 ANSWER 2 OF 9 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 2000090373 MEDLINE
DOCUMENT NUMBER: 20090373 PubMed ID: 10626947
TITLE: Temporal profiles and cellular sources of three nitric oxide synthase isoforms in the brain after experimental contusion.
AUTHOR: Gahm C; Holmin S; Mathiesen T
CORPORATE SOURCE: Department of Clinical Neuroscience, Karolinska Institute, Stockholm, Sweden.
SOURCE: NEUROSURGERY, (2000 Jan) 46 (1) 169-77.
Journal code: 7802914. ISSN: 0148-396X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000209
Last Updated on STN: 20000209
Entered Medline: 20000202

AB OBJECTIVE: Nitric oxide (NO) is a universal mediator of biological effects in the brain. It has been implicated in the pathophysiological processes of traumatic brain injury. Understanding its pathophysiological role in vivo requires an understanding of the cellular sources and tissue compartments of the differentially regulated NO synthase (NOS) isoforms. This study was undertaken to investigate the cellular sources and tissue compartments of NO produced after experimental brain contusions in rats, by analysis of the early expression of the three isoforms of NOS, i.e., the inducible, endothelial, and neuronal isoforms. METHODS: Focal brain contusions were produced in 24 rats using a weight-drop model. The animals were killed 6, 12, 24, 36, or 48 hours after trauma. Sections were analyzed by immunohistochemical and immunofluorescence analyses. Double staining assays were used to define which cells produced the different NOS isoforms. RESULTS: Increases in endothelial NOS-, inducible NOS (iNOS)-, and neuronal NOS-positive cells were detectable by 6 hours after trauma. Endothelial NOS and iNOS levels peaked at 6 and 12 hours, respectively. Expression of neuronal NOS initially increased to a peak at 12 hours but then decreased to a level lower than that in control samples at 36 hours. Endothelial NOS was expressed exclusively in endothelial cells, whereas iNOS was expressed in neutrophils and macrophages. Neuronal NOS was predominantly detected in neurons but was also unexpectedly detected in polymorphonuclear cells. CONCLUSION: In this model, the most striking finding regarding NO-producing enzymes was the expression of iNOS in polymorphonuclear cells and macrophages, cells that invade injured brain tissue. iNOS is thus implicated as a therapeutic target in contusional injuries. This **pattern** of NOS **expression** **cannot** be generalized to all types of brain injuries. The different compartments and cells that can produce NO are differentially regulated; therefore, compartmentalization can explain why NO is beneficial or detrimental, depending on the circumstances. A knowledge of different potential sites and sources of NO is required for any attempts to interfere with the pathophysiological properties of NO.

L34 ANSWER 3 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 3
ACCESSION NUMBER: 1999:464072 BIOSIS
DOCUMENT NUMBER: PREV199900464072
TITLE: Allozyme variation and population genetic structure during the life history of Bufo woodhousii fowleri (Amphibia: Anura.

AUTHOR(S): Hranitz, John M. (1); Diehl, Walter J.
CORPORATE SOURCE: (1) Department of Biology, University of Central Oklahoma, 100 North University Drive, Edmond, OK, 73034 USA
SOURCE: Biochemical Systematics and Ecology, (Jan., 2000) Vol. 28, No. 1, pp. 15-27.
ISSN: 0305-1978.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Allozyme variation in Bufo woodhousii fowleri was assessed to identify unique patterns of expression during the life history of this toad in eastern Mississippi and to determine the toad's population genetic structure. Of 35 loci screened, only five show differential patterns of expression among tissues; three isozymes were expressed differentially during development, and two isozymes showed tissue-specific patterns of expression. Allozyme variation at nine loci showed spatial genetical heterogeneity among breeding sites. Although previous ecological studies indicate a stepping-stone model of population structure for anuran populations which predicts isolation by distance among populations, isolation by distance did not explain population subdivision on the geographic scale of our study. Loci that show differential patterns of gene expression did not contribute any more to population structure than loci that do not show unique **patterns** of gene **expression** . Although we **cannot** eliminate selection as a plausible explanation for the population subdivision we observed, the most likely causes of the genetic heterogeneity among populations of this toad are genetic drift and historical effects. Temporal changes in allele frequencies between the adult and larval cohorts occurred at all the loci studied while there were fewer changes from one life history stage to the next within the cohort. Deviation from Hardy-Weinberg Equilibrium, which occurred at only 25% of the loci showing temporal variation in allele frequencies, was associated with either heterozygote deficiencies or heterozygote excess at different loci.

L34 ANSWER 4 OF 9 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 1998318453 MEDLINE
DOCUMENT NUMBER: 98318453 PubMed ID: 9611151
TITLE: Thyroid receptor plasticity in striated muscle types: effects of altered thyroid state.
AUTHOR: Haddad F; Qin A X; McCue S A; Baldwin K M
CORPORATE SOURCE: Department of Physiology and Biophysics, University of California, Irvine, California 92697, USA.
CONTRACT NUMBER: AR-30346 (NIAMS)
HL-38819 (NHLBI)
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1998 Jun) 274 (6 Pt 1) E1018-26.
Journal code: 0370511. ISSN: 0002-9513.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980817
Last Updated on STN: 20020124
Entered Medline: 19980806

AB This study examined nuclear thyroid receptor (TR) maximum binding capacity (Bmax), dissociation constant (Kd), and TR isoform (alpha1, alpha2, beta1) mRNA expression in rodent cardiac, "fast-twitch white," "fast-twitch red,"

and "slow-twitch red" muscle types as a function of thyroid state. These analyses were performed in the context of slow-twitch type I myosin heavy-chain (MHC) expression, a 3,5,3'-triiodothyronine (T3)-regulated gene that displays varying responsiveness to T3 in the above tissues. Nuclear T3 binding analyses show that the skeletal muscle types express more TRs per unit DNA than cardiac muscle, whereas the latter has a lower Kd than the former. Altered thyroid state had little effect on either cardiac Bmax or Kd, whereas hypothyroidism increased Bmax in the skeletal muscle types without affecting its Kd. Cardiac muscle demonstrated the greatest mRNA signal of TR-beta1 compared with the other muscle types, whereas the TR-alpha1 mRNA signals were more abundant in the skeletal muscle types, especially fast-twitch red. Hyperthyroidism increased the ratio of beta1 to alpha1 and decreased the ratio of alpha2- to alpha1+beta1-mRNA signal across the muscle types, whereas hypothyroidism caused the opposite effects. The nuclear T3 affinity correlated significantly with the TR-beta1 mRNA expression but not with TR-alpha1 mRNA expression. Collectively, these findings suggest that, despite a divergent pattern of TR mRNA expression in the different muscle types, these patterns follow similar qualitative changes under altered thyroid state. Furthermore, TR **expression pattern** **cannot** account for the quantitative and qualitative changes in type I MHC expression that occur in the different muscle types.

L34 ANSWER 5 OF 9 CANCERLIT
ACCESSION NUMBER: 1998318453 CANCERLIT
DOCUMENT NUMBER: 98318453
TITLE: Thyroid receptor plasticity in striated muscle types: effects of altered thyroid state.
AUTHOR: Haddad F; Qin A X; McCue S A; Baldwin K M
CORPORATE SOURCE: Department of Physiology and Biophysics, University of California, Irvine, California 92697, USA.
CONTRACT NUMBER: HL-38819 (NHLBI)
AR-30346 (NIAMS)
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1998). 274 (6 Pt. 1):E1018-26.
Journal code: 3U8. ISSN: 0002-9513.
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
FILE SEGMENT: MEDL; L; Priority Journals
LANGUAGE: English
OTHER SOURCE: MEDLINE 98318453
ENTRY MONTH: 199809
AB This study examined nuclear thyroid receptor (TR) maximum binding capacity
(Bmax), dissociation constant (Kd), and TR isoform (alpha1, alpha2, beta1)
mRNA expression in rodent cardiac, "fast-twitch white," "fast-twitch red,"
and "slow-twitch red" muscle types as a function of thyroid state. These analyses were performed in the context of slow-twitch type I myosin heavy-chain (MHC) expression, a 3,5,3'-triiodothyronine (T3)-regulated gene that displays varying responsiveness to T3 in the above tissues. Nuclear T3 binding analyses show that the skeletal muscle types express more TRs per unit DNA than cardiac muscle, whereas the latter has a lower Kd than the former. Altered thyroid state had little effect on either cardiac Bmax or Kd, whereas hypothyroidism increased Bmax in the skeletal muscle types without affecting its Kd. Cardiac muscle demonstrated the greatest mRNA signal of TR-beta1 compared with the other muscle types, whereas the TR-alpha1 mRNA signals were more abundant in the skeletal muscle types, especially fast-twitch red. Hyperthyroidism increased the ratio of beta1 to alpha1 and decreased the ratio of alpha2- to alpha1+beta1-mRNA signal across the muscle types, whereas hypothyroidism

caused the opposite effects. The nuclear T3 affinity correlated significantly with the TR-beta1 mRNA expression but not with TR-alpha1 mRNA expression. Collectively, these findings suggest that, despite a divergent pattern of TR mRNA expression in the different muscle types, these patterns follow similar qualitative changes under altered thyroid state. Furthermore, TR **expression pattern** **cannot** account for the quantitative and qualitative changes in type I MHC expression that occur in the different muscle types.

L34 ANSWER 6 OF 9 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 1998075900 MEDLINE
DOCUMENT NUMBER: 98075900 PubMed ID: 9415418
TITLE: Lymphocyte subsets and expression of differentiation markers in blood and lymphoid organs of rhesus monkeys.
AUTHOR: Sopper S; Stahl-Hennig C; Demuth M; Johnston I C; Dorries R; ter Meulen V
CORPORATE SOURCE: Institut fur Virologie und Immunbiologie, Universitat Wurzburg, Germany.. viro071@mail.uni-wuerzburg.de
SOURCE: CYTOMETRY, (1997 Dec 1) 29 (4) 351-62.
Journal code: 8102328. ISSN: 0196-4763.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980130
Last Updated on STN: 19980130
Entered Medline: 19980116

AB Rhesus macaques are invaluable experimental animals in biomedical research. Using three color flow cytometry, we screened anti-human antibodies for crossreactivity with macaque cells in order to determine the distribution of functionally important lymphocyte subsets in blood, lymph nodes (LN), and spleen. NK-cells are almost completely absent in LN.
The percentage of B-cells expressing CD80, CD86, and the level of expression of CD20 is higher in blood than in LN. In contrast, a higher proportion of B-cells in LN stains positive for CD21 and CD35. Whereas the
number of CD29hi expressing T-cells is lower, CD69 is expressed on more T-cells in LN than in blood. About one-third of CD8+ T-cells in blood are CD28-, a subset with a unique **pattern** of antigen **expression** which **cannot** be found in LN. In contrast to humans, a relatively high proportion of T-cells in blood also express the co-stimulatory molecules CD80 and CD86. With increasing age, the proportion of B-cells in blood declines, whereas the percentage of T-cells
rises. In addition, the proportion of CD29hi expressing T-cells increases among both the CD4+ and CD8+ subsets.

L34 ANSWER 7 OF 9 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 95291339 MEDLINE
DOCUMENT NUMBER: 95291339 PubMed ID: 7773310
TITLE: A novel Arabidopsis type 1 protein phosphatase is highly expressed in male and female tissues and functionally complements a conditional cell cycle mutant of Aspergillus.
AUTHOR: Arundhati A; Feiler H; Traas J; Zhang H; Lunness P A; Doonan J H
CORPORATE SOURCE: John Innes Centre, Norwich, UK.
SOURCE: PLANT JOURNAL, (1995 May) 7 (5) 823-34.
Journal code: 9207397. ISSN: 0960-7412.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Z46253
ENTRY MONTH: 199507
ENTRY DATE: Entered STN: 19950720
Last Updated on STN: 19950720
Entered Medline: 19950713

AB Type 1 protein phosphatases are very highly conserved throughout eukaryotes where they regulate a number of key metabolic and morphogenetic processes. A cDNA, AtPP1bg, representing a new member of the type 1 protein phosphatase gene family in Arabidopsis has been isolated on the basis of hybridization with the Aspergillus bimG protein phosphatase gene.

The AtPP1bg gene potentially encodes a 37 kDa protein very closely related to PP1 but with divergent N- and C-termini. The predicted amino acid sequence shows 71% identity to the ORF of the bimG gene. When expressed in Aspergillus under the alcA promoter, this phosphatase complements the temperature-sensitive bimG11 mutation allowing nearly normal vegetative growth at 37 degrees C (but not at 42 degrees C). Notably, the plant PP1 does not support morphogenesis (conidiation) at 37 degrees C. This may indicate that conidophore formation has particular phosphatase requirement(s) which the plant PP1 **cannot** supply. The **pattern** of **expression** of the AtPP1bg transcript has been studied during development of the plant. In situ hybridization of Arabidopsis with antisense probes shows that this phosphatase gene is expressed at a low level throughout the plant, but is strongly upregulated within developing flowers, especially in the tapetum, the developing and mature pollen and in the ovaries. This implies that the AtPP1bg either has a specialized role in the formation of these organs, or that there is an increased requirement for protein phosphatase 1 at these stages. It was found that the level of AtPP1bg transcript, as judged by the relative intensity of staining in different cells within the floral meristems, did not vary during the cell cycle.

DUPLICATE 7

L34 ANSWER 8 OF 9 MEDLINE
ACCESSION NUMBER: 91065527 MEDLINE
DOCUMENT NUMBER: 91065527 PubMed ID: 2123468
TITLE: Single cell assay of a transcription factor reveals a threshold in transcription activated by signals emanating from the T-cell antigen receptor.
AUTHOR: Fiering S; Northrop J P; Nolan G P; Mattila P S; Crabtree G R; Herzenberg L A
CORPORATE SOURCE: Department of Genetics, Stanford University, California 94305.
CONTRACT NUMBER: CA39612 (NCI)
CA42509 (NCI)
HL33942 (NHLBI)
SOURCE: GENES AND DEVELOPMENT, (1990 Oct) 4 (10) 1823-34.
Journal code: 8711660. ISSN: 0890-9369.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 199101
ENTRY DATE: Entered STN: 19910308
Last Updated on STN: 19970203
Entered Medline: 19910116

AB Stimulation of T lymphocytes through their antigen receptor leads to the appearance of several transcription factors, including NF-AT and NF-kappa B, which are involved in regulating genes required for immunologic activation. To investigate the activity of a single transcription factor in individual viable cells, we have applied an assay that uses the fluorescence-activated cell sorter to quantitate beta-galactosidase (beta-gal). We have analyzed the distribution of NF-AT transcriptional activity among T cells undergoing activation by using a construct in which three tandem copies of the NF-AT-binding site directs transcription of the lacZ gene. Unexpectedly, stimulation of cloned stably transfected Jurkat T cells leads to a bimodal pattern of beta-gal expression in which some cells express no beta-gal and others express high levels. This **expression pattern cannot** be accounted for by cell-cycle position or heritable variation. Further results, in which beta-gal activity is correlated with NF-AT-binding activity, indicate that the concentration of NF-AT must exceed a critical threshold before transcription initiates. This threshold likely reflects the NF-AT concentration-dependent assembly of transcription complexes at the promoter. Similar constructs controlled by NF-kappa B or the entire interleukin-2 enhancer show bimodal expression patterns during induction, suggesting that thresholds set by the concentration of transcription factors may be a common property of inducible genes.

L34 ANSWER 9 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:428322 BIOSIS
DOCUMENT NUMBER: BA88:86580
TITLE: INTERMEDIATED FILAMENT EXPRESSION AND THE PROGRESSION OF PROSTATIC CANCER AS STUDIED IN THE DUNNING R-3327 RAT PROSTATIC CARCINOMA SYSTEM.
AUTHOR(S): RAMAEKERS F C S; VERHAGEN A P M; ISAACS J T; FEITZ W F J; MOESKER O; SCHAART G; SCHALKEN J A; VOOIJS G P
CORPORATE SOURCE: DEP. PATHOL., UNIV. HOSP. NIJMEGEN, GEERT GROOTEPLEIN ZUID 24, 6525 GA NIJMEGEN, NETH.
SOURCE: PROSTATE, (1989) 14 (4), 323-340.
CODEN: PRSTDS. ISSN: 0270-4137.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB To evaluate if there is any consistent relationship between the expression of intermediate filament proteins (IFP), particularly keratins, and the degree of malignancy of prostatic cancer cells, a series of nine Dunning rat prostatic cancer sublines that span the entire spectrum of progression of prostatic cancer were studied immunocytochemically by the use of a variety of antibodies specific for keratins, vimentin, or desmin. For the keratin studies, monoclonal antibodies with either a general reactivity to several kertins of highly specific for either luminal or basal epithelial cells of the normal rat prostate were used. By use of an antibody specific for luminal cell keratin 18, the luminal tumor cells of the well-differentiated, show-glowing H and HI-S sublines were positively stained. In most of the sublines with a more advanced state of progression

(i.e., the moderately differentiated, moderately fast growing HI-M; the poorly differentiated, faster growing HI-F; and the anaplastic, very fast growing AT-1, AT-2, MAT-Lu tumors), however, no expression of keratin specific for lumnial cells was detected. In addition, several of the most advanced sublines (i.e., AT-1, AT-2, and MAT-Lu) were negative using any of the keratin antibodies. In contrast, several of the other sublines with the most advanced degree of progression (i.e., the anaplastic, very fast growing MAT-LyLu tumor derived from the AT-1 subline; and the anaplastic, very fast growing AT-3 tumor, derived from the HI-F subline), however, were positively stained with the keratin antibody specific for the luminal cells. By use of the keratin antibody specific for the basal cells of the normal rat prostate, the basal tumor cells of the well-differentiated slow-growing H and HI-S tumor were positively stained. This positive staining for basal cell keratin was also found in the HI0-M and HI-G tumors, while the AT-1, AT-2, MAT-Lu, MAT-LyLu, and AT-3 were negative with this antibody. Thus, a loss in staining for basal cell keratin was consistently associated with the most advanced state of tumor progression.

Vimentin-positive staining was demonstrated either alone or with keratin-positive staining in part of the epithelial cancer cells of all the sublines. An increase in the positive staining for vimentin was consistently associated with a more advanced state of tumor progression. Desmin-positive staining was found only in smooth cells present within the various tumor sublines. These studies have demonstrated that different sublines of the Dunning prostatic cancer system can be distinguished on the basis of their pattern of intermediate filament protein expression and that these patterns are subject to dynamic regulation (both positive and negative) during the progression of prostatic cancer. Unfortunately, the **pattern** of IFP **expression cannot** be used alone to predict the metastatic ability of prostatic cancer.

=> d history

(FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002)

FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002

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L1          168 S ORTHOLOG AND PY<1998
L2          106 S ORTHOLOG AND PY<1997
L3           65 S ORTHOLOG AND PY<1996
L4           42 S ORTHOLOG AND PY<1995
L5           27 S ORTHOLOG AND PY<1994
L6           21 S ORTHOLOG AND PY<1993
L7           15 S ORTHOLOG AND PY<1992
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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT 15:19:03 ON 09 JUL 2002

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L8       350284 S YAN?/AU
L9            0 S L8 AND NADRIN#
L10          26 S L8 AND (RAS(W)LIKE)
L11        1054 S KETCHUM?/AU
L12        1550 S (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13        4464 S BEASLEY?/AU
L14        6870 S L11 OR L12 OR L13
L15           0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
L16          10 DUP REM L10 (16 DUPLICATES REMOVED)
L17         164 S L8 AND (VIRTUAL)
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L18           0 S L8 AND (VIRTUAL(3A)NORTHERN)
L19           0 S L14 AND (VIRTUAL(3A)NORTHERN)
L20      266508 S (MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#)(3A)EXPRESS?
L21      336550 S (PROTEIN# OR PEPTIDE# OR TRANSLAT?)(3A)EXPRESS?
L22       37711 S L20(S)L21
L23      183803 S EST OR ESTS OR (EXPRESSED(3W)TAG#)
L24         286 S L22(S)L23
L25         100 S L24(S)DATABASE#
L26          35 DUP REM L25 (65 DUPLICATES REMOVED)
L27           0 S ("IN"(W)SILICO) AND (VIRTUAL(2A)NORTHERN)
L28         146 S ("IN"(W)SILICO) OR (VIRTUAL(2A)NORTHERN)
L29           8 S L28 AND (EXPRESS?(2A)PATTERN#)
L30           8 DUP REM L29 (0 DUPLICATES REMOVED)
L31           1 S L28 AND ("NOT" OR CANNOT)
L32       84350 S (EXPRESSION(2A)PATTERN#)
L33          21 S L32(2A)CANNOT
L34           9 DUP REM L33 (12 DUPLICATES REMOVED)

=> s l32(3a)predict?
L35         224 L32(3A) PREDICT?

=> s l32(3a)("not"(2a)predict?)
L36           0 L32(3A)("NOT"(2A) PREDICT?)

=> s l32(3a)("not"(3a)predict?)
L37           0 L32(3A)("NOT"(3A) PREDICT?)

=> s l32(3a)("not")
L38           1 L32(3A)("NOT")

=> d ibib abs

L38  ANSWER 1 OF 1  BIOSIS  COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER:    2001:430688  BIOSIS
DOCUMENT NUMBER:     PREV200100430688
TITLE:               Cloning and embryonic expression of organizer-related
genes
                     in amphioxus, Branchiostoma belcheri.
AUTHOR(S):           Wang, Yong (1); Masai, Ichiro; Yasui, Kinya; Zhang,
Peijun;
                     Saiga, Hidetoshi (1)
CORPORATE SOURCE:    (1) Tokyo Metropolitan University, Hachioji, Tokyo Japan
SOURCE:              Development Growth & Differentiation, (July, 2001) Vol.
43,
                     No. Supplement, pp. S69. print.
                     Meeting Info.: 14th International Congress of
Developmental
                     biology Kyoto, Japan July 08-12, 2001
                     ISSN: 0012-1592.
DOCUMENT TYPE:       Conference
LANGUAGE:            English
SUMMARY LANGUAGE:    English


=> l28 and (drawnback# or shortcoming# or fail?)
L28 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l28 and (drawnback# or shortcoming# or fail?)
```

L39 4 L28 AND (DRAWNBACK# OR SHORTCOMING# OR FAIL?)

=> dup rem l39
PROCESSING COMPLETED FOR L39
L40 4 DUP REM L39 (0 DUPLICATES REMOVED)

=> d ibib abs tot

L40 ANSWER 1 OF 4 MEDLINE
ACCESSION NUMBER: 2002189769 MEDLINE
DOCUMENT NUMBER: 21920197 PubMed ID: 11922955
TITLE: Computer systems for the prediction of xenobiotic metabolism.
AUTHOR: Langowski Jan; Long Anthony
CORPORATE SOURCE: LHASA Limited, School of Chemistry, University of Leeds, Woodhouse Lane, LS2 9JT, West Yorkshire, UK.
SOURCE: Adv Drug Deliv Rev, (2002 Mar 31) 54 (3) 407-15. Ref: 31
Journal code: 8710523. ISSN: 0169-409X.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020522
Entered Medline: 20020521

AB The aim of pharmaceutical research and development is to ensure a continuing pipeline of new chemical entities (NCEs) displaying high therapeutic efficacy with few or no side effects. **Failure** of promising lead candidates late in the drug discovery processes is regarded as commercially unacceptable in today's increasingly competitive business environment. An inappropriate ADME/Toxicity profile in humans is the major cause of **failure** of lead candidates in late clinical stages of drug development. Combinatorial chemistry techniques coupled with high throughput screening protocols means that pharmaceutical companies are now dealing with an unprecedented number of NCEs on an annual basis. As a consequence, screening for undesirable ADME/Toxicity properties in the early stages of drug development, preferably pre-synthesis, is now considered the essential paradigm. **In silico** assessment of NCEs is rapidly emerging as the next wave of technology for early ADME/Toxicity prediction. In this review, we discuss the major commercially available products for the assessing the potential metabolic activity of xenobiotic substances in mammalian systems.

L40 ANSWER 2 OF 4 MEDLINE
ACCESSION NUMBER: 2001522882 MEDLINE
DOCUMENT NUMBER: 21454105 PubMed ID: 11570367
TITLE: "**In silico** experiments"--yes, but the great western cowboy "random chance" is still alive.
COMMENT: Comment on: Fertil Steril. 2000 Dec;74(6):1108-13
Comment in: Fertil Steril. 2001 Sep;76(3):639-40
AUTHOR: Sher G; Fisch J D
SOURCE: FERTILITY AND STERILITY, (2001 Sep) 76 (3) 636-7; discussion 638-9.
Journal code: 0372772. ISSN: 0015-0282.
PUB. COUNTRY: United States

Commentary
Letter
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010926
Last Updated on STN: 20020419
Entered Medline: 20011011

L40 ANSWER 3 OF 4 MEDLINE
ACCESSION NUMBER: 2001522883 MEDLINE
DOCUMENT NUMBER: 21454106 PubMed ID: 11570368
TITLE: "**In silico** experiments"--yes, but the great western cowboy "random chance" is still alive.
COMMENT: Comment on: Fertil Steril. 1994 Feb;61(2):248-51
Comment on: Fertil Steril. 2000 Dec;74(6):1108-13
Comment on: Fertil Steril. 2000 Mar;73(3):536-40
Comment in: Fertil Steril. 2001 Sep;76(3):639-40
AUTHOR: Stricker R B; Steinleitner A
SOURCE: FERTILITY AND STERILITY, (2001 Sep) 76 (3) 637-9.
Journal code: 0372772. ISSN: 0015-0282.
PUB. COUNTRY: United States
Commentary
Letter
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010926
Last Updated on STN: 20020419
Entered Medline: 20011011

L40 ANSWER 4 OF 4 MEDLINE
ACCESSION NUMBER: 2001075841 MEDLINE
DOCUMENT NUMBER: 20408884 PubMed ID: 10950924
TITLE: C21orf5, a novel human chromosome 21 gene, has a Caenorhabditis elegans ortholog (pad-1) required for embryonic patterning.
AUTHOR: Guipponi M; Brunschwig K; Chamoun Z; Scott H S; Shibuya K; Kudoh J; Delezoide A L; El Samadi S; Chettouh Z; Rossier C;
Shimizu N; Mueller F; Delabar J M; Antonarakis S E
CORPORATE SOURCE: Division of Medical Genetics, University and Cantonal Hospital, 1 rue Michel Servet, Geneva 4, 1211, Switzerland.
SOURCE: GENOMICS, (2000 Aug 15) 68 (1) 30-40.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ237839; GENBANK-AJ250261
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010111

AB To contribute to the development of the transcription map of human chromosome 21 (HC21), we isolated a new transcript, C21orf5 (chromosome 21 open reading frame 5), encoding a predicted 2298-amino-acid protein. Analysis of the genomic DNA sequence revealed that C21orf5 consists of 37 exons that extend over 130 kb and maps between the CBR3 (carbonyl

reductase 3) and the KIAA0136 genes. Northern blot analyses showed a ubiquitously expressed RNA species of 8.5 kb. RNA in situ hybridization on brain sections of normal human embryos revealed a strong labeling in restricted areas of the cerebral cortex. **In silico** analysis of the deduced C21orf5 protein revealed several highly probable transmembrane segments but no known protein domains or homology with known proteins. However, there were significant homologies to several hypothetical Caenorhabditis elegans proteins and Drosophila melanogaster genomic sequences. To investigate the function of C21orf5, we isolated the cDNA of the C. elegans ortholog and performed double-stranded RNA-mediated genetic interference experiments. The major phenotype observed in the progeny of injected animals was embryonic lethality. Most of the tissues of the embryo **failed** to undergo proper patterning during gastrulation, and morphogenesis did not occur; thus we termed the ortholog pad-1, for patterning defective 1. These results indicated that pad-1 is essential for the development and the survival of C. elegans. This study provides the first example of the use of C. elegans as a model to study the function of genes on human chromosome 21 that might be involved in Down syndrome.

=> d history

(FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002)

FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002

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L1          168 S ORTHOLOG AND PY<1998
L2          106 S ORTHOLOG AND PY<1997
L3           65 S ORTHOLOG AND PY<1996
L4           42 S ORTHOLOG AND PY<1995
L5           27 S ORTHOLOG AND PY<1994
L6           21 S ORTHOLOG AND PY<1993
L7           15 S ORTHOLOG AND PY<1992
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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT 15:19:03 ON 09 JUL 2002

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L8       350284 S YAN?/AU
L9            0 S L8 AND NADRIN#
L10          26 S L8 AND (RAS(W)LIKE)
L11        1054 S KETCHUM?/AU
L12        1550 S (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13        4464 S BEASLEY?/AU
L14        6870 S L11 OR L12 OR L13
L15           0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
L16          10 DUP REM L10 (16 DUPLICATES REMOVED)
L17         164 S L8 AND (VIRTUAL)
L18           0 S L8 AND (VIRTUAL(3A)NORTHERN)
L19           0 S L14 AND (VIRTUAL(3A)NORTHERN)
L20      266508 S (MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#)(3A)EXPRESS?
L21      336550 S (PROTEIN# OR PEPTIDE# OR TRANSLAT?)(3A)EXPRESS?
L22       37711 S L20(S)L21
L23      183803 S EST OR ESTS OR (EXPRESSED(3W)TAG#)
L24         286 S L22(S)L23
L25         100 S L24(S)DATABASE#
L26          35 DUP REM L25 (65 DUPLICATES REMOVED)
```

```
L27           0 S ("IN"(W)SILICO) AND (VIRTUAL(2A)NORTHERN)
L28         146 S ("IN"(W)SILICO) OR (VIRTUAL(2A)NORTHERN)
L29           8 S L28 AND (EXPRESS?(2A)PATTERN#)
L30           8 DUP REM L29 (0 DUPLICATES REMOVED)
L31           1 S L28 AND ("NOT" OR CANNOT)
L32       84350 S (EXPRESSION(2A)PATTERN#)
L33          21 S L32(2A)CANNOT
L34           9 DUP REM L33 (12 DUPLICATES REMOVED)
L35         224 S L32(3A)PREDICT?
L36           0 S L32(3A)("NOT"(2A)PREDICT?)
L37           0 S L32(3A)("NOT"(3A)PREDICT?)
L38           1 S L32(3A)("NOT")
L39           4 S L28 AND (DRAWNBACK# OR SHORTCOMING# OR FAIL?)
L40           4 DUP REM L39 (0 DUPLICATES REMOVED)

=> s cannot(3w)(rely or relied)
L41         929 CANNOT(3W)(RELY OR RELIED)

=> s l32 (s)l41
L42           0 L32 (S) L41

=> s l23(s)l41
L43           3 L23(S) L41

=> d ibib abs tot

L43  ANSWER 1 OF 3  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         2001:683510  CAPLUS
DOCUMENT NUMBER:          136:275383
TITLE:                    Biological indicators for the identification of
                          ionizing radiation exposure in humans
AUTHOR(S):                Amundson, Sally A.; Bittner, Michael; Meltzer, Paul;
                          Trent, Jeffrey; Fornace, Albert J., Jr.
CORPORATE SOURCE:         NIH, National Cancer Institute, Bethesda, MD, 20892,
                          USA
SOURCE:                   Expert Review of Molecular Diagnostics (2001), 1(2),
                          211-219
                          CODEN: ERMDCW; ISSN: 1473-7159
PUBLISHER:                Future Drugs Ltd.
DOCUMENT TYPE:            Journal; General Review
LANGUAGE:                 English
AB   A review.  While the effects of acute high-dose irradn. are
     well-documented, less is known about the effects of low level chronic
     radiation exposure.  Phys. dosimetry cannot always be
     relied upon, so dose ests. and detn. of past radiation
     exposure must often be based upon biol. indicators.  Some of the
     established methods used in the assessment of nuclear accidents are
     reviewed here, including cytogenetic analyses, mutation-based assays and
     ESR.  As interest in research on low-level radiation exposures expands,
     there is an increasing need for new biomarkers that can identify exposed
     individuals in human populations.  Developments in high-throughput gene
     expression profiling may enable future development of a rapid and
     noninvasive testing method for application to potentially exposed
     populations.
REFERENCE COUNT:          52    THERE ARE 52 CITED REFERENCES AVAILABLE FOR
THIS
                                RECORD. ALL CITATIONS AVAILABLE IN THE RE

FORMAT

L43  ANSWER 2 OF 3  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         1996:26169  CAPLUS
```

DOCUMENT NUMBER: 124:96437
TITLE: Use of a simple titration procedure to determine H2CO3 alkalinity and volatile fatty acids for process control in waste-water treatment
AUTHOR(S): de Haas, D W; Adam, N
CORPORATE SOURCE: Umgeni Water, Pietermaritzburg, 3200, S. Afr.
SOURCE: Water SA (1995), Volume Date 1995, 21(4), 307-18
CODEN: WASADV; ISSN: 0378-4738
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A simple 5-pH point titrimetric method developed elsewhere was tested for measurement of bicarbonate (or H2CO3*) alky. and volatile fatty acids (VFA) in primary sludge, fermented primary sludge or its supernatant, settled sewage, and anaerobic digester sludge (under process failure conditions). The titrimetric method incorporates a computer program to calc. the necessary results from a modified Gran titrn. in the presence of known concns. of phosphate and ammonia. Comparisons were made between the titrimetric method, a colorimetric method, and an HPLC method for VFA detn. The value of the titrimetric H2CO3* alky. result compared to that of conventional methods for anaerobic digester samples was also investigated. The results indicated good overall agreement between the three methods of VFA detn. From statistical anal., the titrimetric method was found to overpredict the VFA content of failed anaerobic digester samples by approx. 15%, relative to the colorimetric method. Statistical agreement between the titrimetric and HPLC methods for these samples was good, provided the high frequency of outliers (.apprx.20% of the data pairs rejected) was taken into account. No immediate explanation for the deviations between the methods for failed anaerobic digester samples could be found. However, from the point of view of method simplicity and avoidance of inherent pitfalls in other methods of H2CO3* alky. estn., the titrimetric method gave very useful results in process control and chem. dosing during start-up of two full-scale anaerobic digesters. The potential value of the titrimetric method for process control of primary sludge fermn. in biol. nutrient removal plants was also highlighted. Although problems were encountered with reaching the lower detection limits of all three methods, the results for settled sewage suggest that the titrimetric method can give a fairly reliable est. of VFA, even at low concns. Using the titrimetric method, good recovery of VFA from spiked samples of settled sewage in the range 40 to 80 mg/L as acetic acid was obtained. Using pure solns. of carbonate and acetate, the detection limits for the titrimetric method were found to be approx. 10 mg/L as CaCO3 and 5 mg/L as acetic acid. Scrupulous attention to pH probe maintenance and calibration was found to be an essential requirement for use of the titrimetric method, particularly at low concns. when the systematic pH error **est**. by the computer program **cannot** be **relied** upon.

L43 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1969:108959 CAPLUS
DOCUMENT NUMBER: 70:108959
TITLE: Evaluation of a colorimetric personal dosimeter for hydrazine fuels
AUTHOR(S): Arnold, Eugene L.; Rakowski, Robert F.
CORPORATE SOURCE: Aerosp. Med. Res. Lab., Wright-Patterson Air Force

Base, Ohio, USA
SOURCE: U.S. Clearinghouse Fed. Sci. Tech. Inform., AD (1968),
AD-679527, 29 pp. Avail.: CFSTI
From: U. S. Govt. Res. Develop. Rep. 1969, 69(4), 54
CODEN: XCCIAV
DOCUMENT TYPE: Report
LANGUAGE: English

AB An evaluation of the performance of the colorimetric personal dosimeter for hydrazine fuels was conducted. The dosimeter reagent is an acid-base indicator. Volatile bases give false pos. results, and acids decrease the sensitivity of the strips to hydrazines. The useful shelf life of unopened dosimeter packets is >1 year. Variations in sensitivity were observed for different lots of dosimeter strips. This problem can be corrected by proper quality control. The majority of the strips were more sensitive than indicated by the manufacturer's calibration. Variation in the concn. (C) and time of exposure (T) at a const. CT product had little effect on the darkness of the strip but considerable effect on the hue. Strips placed in a closed cabinet for 8 hrs. developed a slightly red color. The badge is useful primarily as a check on the continued safety of areas which were surveyed by a qualified bioenvironmental engineer. The badge **cannot** be **relied** on to give a useful **est**. of the dose received in the case of a gross overexposure. The badge is a sensitive detector for hydrazine fuels. No great dependence should be placed on the quant. interpretation of the colors developed.

=> d history

(FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002)

FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002
L1 168 S ORTHOLOG AND PY<1998
L2 106 S ORTHOLOG AND PY<1997
L3 65 S ORTHOLOG AND PY<1996
L4 42 S ORTHOLOG AND PY<1995
L5 27 S ORTHOLOG AND PY<1994
L6 21 S ORTHOLOG AND PY<1993
L7 15 S ORTHOLOG AND PY<1992

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT 15:19:03 ON 09 JUL 2002
L8 350284 S YAN?/AU
L9 0 S L8 AND NADRIN#
L10 26 S L8 AND (RAS(W)LIKE)
L11 1054 S KETCHUM?/AU
L12 1550 S (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13 4464 S BEASLEY?/AU
L14 6870 S L11 OR L12 OR L13
L15 0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
L16 10 DUP REM L10 (16 DUPLICATES REMOVED)
L17 164 S L8 AND (VIRTUAL)
L18 0 S L8 AND (VIRTUAL(3A)NORTHERN)
L19 0 S L14 AND (VIRTUAL(3A)NORTHERN)
L20 266508 S (MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#)(3A)EXPRESS?
L21 336550 S (PROTEIN# OR PEPTIDE# OR TRANSLAT?)(3A)EXPRESS?
L22 37711 S L20(S)L21
L23 183803 S EST OR ESTS OR (EXPRESSED(3W)TAG#)

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L24          286 S L22(S)L23
L25          100 S L24(S)DATABASE#
L26           35 DUP REM L25 (65 DUPLICATES REMOVED)
L27            0 S ("IN"(W)SILICO) AND (VIRTUAL(2A)NORTHERN)
L28          146 S ("IN"(W)SILICO) OR (VIRTUAL(2A)NORTHERN)
L29            8 S L28 AND (EXPRESS?(2A)PATTERN#)
L30            8 DUP REM L29 (0 DUPLICATES REMOVED)
L31            1 S L28 AND ("NOT" OR CANNOT)
L32        84350 S (EXPRESSION(2A)PATTERN#)
L33           21 S L32(2A)CANNOT
L34            9 DUP REM L33 (12 DUPLICATES REMOVED)
L35          224 S L32(3A)PREDICT?
L36            0 S L32(3A)("NOT"(2A)PREDICT?)
L37            0 S L32(3A)("NOT"(3A)PREDICT?)
L38            1 S L32(3A)("NOT")
L39            4 S L28 AND (DRAWNBACK# OR SHORTCOMING# OR FAIL?)
L40            4 DUP REM L39 (0 DUPLICATES REMOVED)
L41          929 S CANNOT(3W)(RELY OR RELIED)
L42            0 S L32 (S)L41
L43            3 S L23(S)L41

=> s database#
L44      116057 DATABASE#

=> s l44(s)l41
L45            3 L44(S) L41

=> d ibib abs tot

L45  ANSWER 1 OF 3      MEDLINE
ACCESSION NUMBER:    2002199848      IN-PROCESS
DOCUMENT NUMBER:     21930277   PubMed ID: 11932440
TITLE:               Potassium- or sodium-efflux ATPase, a key enzyme in the
                     evolution of fungi.
AUTHOR:              Benito Begona; Garciadeblas Blanca; Rodriguez-Navarro
                     Alonso
CORPORATE SOURCE:    Departamento de Biotecnologia, Escuela Tecnica Superior de
                     Ingenieros Agronomos, Universidad Politecnica de Madrid,
                     28040 Madrid, Spain.
SOURCE:              MICROBIOLOGY, (2002 Apr) 148 (Pt 4) 933-41.
                     Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY:        England: United Kingdom
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE:          Entered STN: 20020405
                     Last Updated on STN: 20020405
AB   Potassium is the most abundant cation in cells. Therefore,
     plant-associated fungi and intracellular parasites are permanently or
     circumstantially exposed to high K(+) and must avoid excessive K(+)
     accumulation activating K(+) efflux systems. Because high K(+) and high
pH
     are compatible in natural environments, free-living organisms cannot keep
     a permanent transmembrane DeltapH and cannot rely only
     on K(+)/H(+) antiporters, as do mitochondria. This study shows that the
     Schizosaccharomyces pombe CTA3 is a K(+)-efflux ATPase, and that other
     fungi are furnished with Na(+)-efflux ATPases, which also pump Na(+). All
     these fungal ATPases, including those pumping only Na(+), form a
     phylogenetic group, IID or ENA, among P-type ATPases. By searching in
     databases and partial cloning of ENA genes in species of
     Zygomycetes and Basidiomycetes, the authors conclude that probably all
```

fungi have these genes. This study indicates that fungal K(+)- or Na(+)-ATPases evolved from an ancestral K(+)-ATPase, through processes of gene duplication. In yeast hemiascomycetes these duplications have occurred recently and produced bifunctional ATPases, whereas in Neurospora, and probably in other euascomycetes, they occurred earlier in evolution and produced specialized ATPases. In Schizosaccharomyces, adaptation to Na(+) did not involve the duplication of the K(+)-ATPase and thus it retains an enzyme which is probably close to the original one. The parasites Leishmania and Trypanosoma have ATPases phylogenetically related to fungal K(+)-ATPases, which are probably functional homologues of the fungal enzymes.

L45 ANSWER 2 OF 3 MEDLINE
ACCESSION NUMBER: 2001308011 MEDLINE
DOCUMENT NUMBER: 20495602 PubMed ID: 11040727
TITLE: Supervised physical activity in Sweden: in theory and practice.
AUTHOR: Hjalmarson A; Rossner S; Ostenson C G
CORPORATE SOURCE: Obesity Unit, Huddinge University Hospital, Sweden.
SOURCE: PATIENT EDUCATION AND COUNSELING, (2000 Feb) 39 (2-3) 281-4.
Journal code: 8406280. ISSN: 0738-3991.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Nursing Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010604
Last Updated on STN: 20010604
Entered Medline: 20010531

AB The aim of this study was to assess to which extent community-run projects including physical activity could be identified, described and analysed in terms of objectives, organisation, evaluation and financing, as a resource in prevention and treatment of common lifestyle-related medical problems. The Swedish **database** Spriline was used as a main source of information. Identification of ongoing Swedish activities was followed by a mail questionnaire. In total, 151 projects were eventually identified. A semistructured questionnaire containing about 30 questions was mailed to the individual listed as responsible for the project, with a reminder 2 months later. Only 52 projects were viable; a follow-up of nonresponders showed that no relevant activity program had ever existed or that the person responsible had left. Walking, aerobics and water activities were the dominating types of activity. Most projects addressed both sexes, but eight weight reduction programs were designed for women only. Evaluation ranged from 'measuring attendance' to 'scientific evaluation'. Physical activity programs may not be as systematically organised as the Swedish **database** suggests and **cannot** generally be **relied** upon as support in patient care, unless critically evaluated in advance.

L45 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:305189 BIOSIS
DOCUMENT NUMBER: PREV200200305189
TITLE: Potassium- or sodium-efflux ATPase, a key enzyme in the evolution of fungi.

AUTHOR(S): Benito, Begona; Garciadeblas, Blanca; Rodriguez-Navarro, Alonso (1)

CORPORATE SOURCE: (1) Departamento de Biotechnologia, Escuela Tecnica Superior de Ingenieros Agronomos, Universidad Politecnica de Madrid, 28040, Madrid: arodrignavar@bit.etsia.upm.es Spain

SOURCE: Microbiology (Reading), (April, 2002) Vol. 148, No. 4, pp. 933-941. print.
ISSN: 1350-0872.

DOCUMENT TYPE: Article
LANGUAGE: English

AB Potassium is the most abundant cation in cells. Therefore, plant-associated fungi and intracellular parasites are permanently or circumstantially exposed to high K+ and must avoid excessive K+ accumulation activating K+ efflux systems. Because high K+ and high pH are compatible in natural environments, free-living organisms cannot keep a permanent transmembrane DELTApH and **cannot rely** only on K+/H+ antiporters, as do mitochondria. This study shows that the Schizosaccharomyces pombe CTA3 is a K+-efflux ATPase, and that other fungi are furnished with Na+-efflux ATPase, which also pump Na+. All these fungal ATPases, including those pumping only Na+, form a phylogenetic group, IID or ENA, among P-type ATPases. By searching in **databases** and partial cloning of ENA genes in species of Zygomycetes and Basidiomycetes, the authors conclude that probably all fungi have these genes. This study indicates that fungal K+- or Na+-ATPases evolved from an ancestral K+-ATPase, through processes of gene duplication. In yeast hemiascomycetes these duplications have occurred recently and produced bifunctional ATPases, whereas in Neurospora, and probably in other euascomycetes, they occurred earlier in evolution and produced specialized ATPases. In Schizosaccharomyces, adaptation to Na+ did not involve the duplication of the K+-ATPase and thus it retains an enzyme which is probably close to the original one. The parasites Leishmania and Trypanosoma have ATPases phylogenetically related to fungal H+-ATPases, which are probably functional homologues of the fungal enzymes.

=> d history

(FILE 'HOME' ENTERED AT 15:02:56 ON 09 JUL 2002)

FILE 'MEDLINE' ENTERED AT 15:03:04 ON 09 JUL 2002

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L1          168 S ORTHOLOG AND PY<1998
L2          106 S ORTHOLOG AND PY<1997
L3           65 S ORTHOLOG AND PY<1996
L4           42 S ORTHOLOG AND PY<1995
L5           27 S ORTHOLOG AND PY<1994
L6           21 S ORTHOLOG AND PY<1993
L7           15 S ORTHOLOG AND PY<1992
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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT 15:19:03 ON 09 JUL 2002

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L8       350284 S YAN?/AU
L9            0 S L8 AND NADRIN#
L10          26 S L8 AND (RAS(W)LIKE)
L11        1054 S KETCHUM?/AU
L12        1550 S (DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13        4464 S BEASLEY?/AU
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L14          6870 S L11 OR L12 OR L13
L15             0 S L14 AND (NADRIN# OR (RAS(W)LIKE))
L16            10 DUP REM L10 (16 DUPLICATES REMOVED)
L17           164 S L8 AND (VIRTUAL)
L18             0 S L8 AND (VIRTUAL(3A)NORTHERN)
L19             0 S L14 AND (VIRTUAL(3A)NORTHERN)
L20        266508 S (MRNA OR CDNA OR POLYNUCLEOTIDE# OR TRANSCRIPT#)(3A)EXPRESS?
L21        336550 S (PROTEIN# OR PEPTIDE# OR TRANSLAT?)(3A)EXPRESS?
L22         37711 S L20(S)L21
L23        183803 S EST OR ESTS OR (EXPRESSED(3W)TAG#)
L24           286 S L22(S)L23
L25           100 S L24(S)DATABASE#
L26            35 DUP REM L25 (65 DUPLICATES REMOVED)
L27             0 S ("IN"(W)SILICO) AND (VIRTUAL(2A)NORTHERN)
L28           146 S ("IN"(W)SILICO) OR (VIRTUAL(2A)NORTHERN)
L29             8 S L28 AND (EXPRESS?(2A)PATTERN#)
L30             8 DUP REM L29 (0 DUPLICATES REMOVED)
L31             1 S L28 AND ("NOT" OR CANNOT)
L32         84350 S (EXPRESSION(2A)PATTERN#)
L33            21 S L32(2A)CANNOT
L34             9 DUP REM L33 (12 DUPLICATES REMOVED)
L35           224 S L32(3A)PREDICT?
L36             0 S L32(3A)("NOT"(2A)PREDICT?)
L37             0 S L32(3A)("NOT"(3A)PREDICT?)
L38             1 S L32(3A)("NOT")
L39             4 S L28 AND (DRAWNBACK# OR SHORTCOMING# OR FAIL?)
L40             4 DUP REM L39 (0 DUPLICATES REMOVED)
L41           929 S CANNOT(3W)(RELY OR RELIED)
L42             0 S L32 (S)L41
L43             3 S L23(S)L41
L44        116057 S DATABASE#
L45             3 S L44(S)L41

=> s anticipat?(s)l32
L46           139 ANTICIPAT?(S) L32

=> s anticipat?(5a)l32
L47            14 ANTICIPAT?(5A) L32

=> dup rem l47
PROCESSING COMPLETED FOR L47
L48             6 DUP REM L47 (8 DUPLICATES REMOVED)

=> d ibib abs tot

L48  ANSWER 1 OF 6  LIFESCI    COPYRIGHT 2002 CSA
ACCESSION NUMBER:   2001:66499  LIFESCI
TITLE:              Switching nucleic acids for antibodies
AUTHOR:             Hoffman, D.; Hesselberth, J.; Ellington, A.D.*
CORPORATE SOURCE:   Department of Chemistry and Biochemistry, Institute for
                    Cellular and Molecular Biology, University of Texas at
                    Austin, Austin, TX 78712, USA; E-mail:
                    andy.ellington@mail.utexas.edu
SOURCE:             Nature Biotechnology [Nat. Biotechnol.], (20010400) vol.
                    19, no. 4, pp. 313-314.
                    ISSN: 1087-0156.
DOCUMENT TYPE:      Journal
TREATMENT CODE:     General Review
FILE SEGMENT:       W3
LANGUAGE:           English
AB   The development of DNA arrays has revealed a wealth of information about
```

gene **expression patterns**. It is widely **anticipated** that a similar glut of information about the concentrations and modification states of cellular proteins and metabolites will soon become available as a result of the development of similar array formats for proteomics and metabolomics. Although it is difficult to predict exactly when or how such arrays will first be generated, it is nonetheless reasonable to expect that just as synthetic oligonucleotides and complementary DNAs served as all-purpose receptors for messenger RNAs and their fluorescent derivatives, antibodies may well serve as all-purpose receptors for proteins and metabolites. Indeed, recent results from Brown and colleagues provide a glimpse of how large-scale antibody arrays may soon be used to quantify levels of serum proteins.

L48 ANSWER 2 OF 6 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2001037967 MEDLINE
DOCUMENT NUMBER: 20419860 PubMed ID: 10963870
TITLE: Steroidogenic factor 1 (SF-1) is essential for ovarian development and function.
AUTHOR: Hanley N A; Ikeda Y; Luo X; Parker K L
CORPORATE SOURCE: Departments of Internal Medicine and Pharmacology, University of Texas Southwestern Medical Center, Dallas, TX
75235-8857, USA.
CONTRACT NUMBER: HL 48460 (NHLBI)
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (2000 May 25) 163 (1-2) 27-32. Ref: 31
Journal code: 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001128

AB The orphan nuclear receptor steroidogenic factor 1 (SF-1) was identified originally as a key regulator of the tissue-specific expression of the cytochrome P450 steroid hydroxylases. Hints at considerably broader roles for SF-1 came from analyses of its **expression pattern** in mouse embryos. As **anticipated**, SF-1 was expressed in the adrenal glands and gonads from their early stages of development. Surprisingly, SF-1 also was expressed outside of the primary steroidogenic tissues in the anterior pituitary and hypothalamus. SF-1 knockout mice dramatically confirmed its multiple essential roles in vivo. These mice lacked adrenal glands and gonads, leading to adrenocortical insufficiency and male-to-female sex reversal of their internal and external genitalia. SF-1 knockout mice also had impaired pituitary expression of gonadotropins and agenesis of the ventromedial hypothalamic nucleus (VMH), confirming roles of SF-1 at all three levels of the hypothalamic-pituitary-gonadal axis. With some focus on the ovary, this review summarizes experiments that have defined essential roles of SF-1 in endocrine development, and highlights important areas for future studies.

L48 ANSWER 3 OF 6 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1999141329 MEDLINE
DOCUMENT NUMBER: 99141329 PubMed ID: 9973545

TITLE: Expression patterns of folate binding proteins one and two in the developing mouse embryo.
AUTHOR: Barber R C; Bennett G D; Greer K A; Finnell R H
CORPORATE SOURCE: Department of Veterinary Anatomy and Public Health, Texas A&M University, College Station, Texas, 77843-4458, USA.
CONTRACT NUMBER: ES07165 (NIEHS)
HD/ES35396 (NICHD)
P30-E509106
SOURCE: MOLECULAR GENETICS AND METABOLISM, (1999 Jan) 66 (1) 31-9.
Journal code: 9805456. ISSN: 1096-7192.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 19990324
Entered Medline: 19990311

AB Expression patterns of mRNAs coding for the murine folate binding proteins one and two (FBP1 and FBP2) were determined by ribonuclease protection assay (RPA) in highly inbred SWV/Fnn mouse embryos. Tissue samples for RPA were collected from the anterior neural tube throughout the period of embryonic development, as well as from maternal- and fetal-derived term placenta. The peak in expression of FBP1 occurred in term placental tissue compared to neural tissue from any time point. This relative increase in FBP1 expression occurred in placental tissue of embryonic, as opposed to maternal, origin. The expression of FBP2 did not differ statistically between any timepoints or tissues examined. Expression of both FBP1 and FBP2 was slightly elevated throughout the period of neural tube closure (Gestational Days 8 through 10), although not significantly. These data fit the **anticipated expression patterns** of the homologues of human folate receptors alpha and beta, thus helping to resolve some of the confusion secondary to the nomenclature associated with this gene family. Furthermore, the expression of these two genes in the neural tube closure stage of embryological development supports their involvement in regulatory events related to normal neural tube morphogenesis.

L48 ANSWER 4 OF 6 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1999077301 MEDLINE
DOCUMENT NUMBER: 99077301 PubMed ID: 9862485
TITLE: Promoter trapping identifies real genes in C. elegans.
AUTHOR: Hope I A; Arnold J M; McCarroll D; Jun G; Krupa A P; Herbert R
CORPORATE SOURCE: School of Biology, The University of Leeds, UK..
i.a.hope@leeds.ac.uk
SOURCE: MOLECULAR AND GENERAL GENETICS, (1998 Nov) 260 (2-3) 300-8.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199901
ENTRY DATE: Entered STN: 19990128
Last Updated on STN: 19990128
Entered Medline: 19990114

AB Promoter trapping involved screening uncharacterized fragments of C. elegans genomic DNA for C. elegans promoter activity. By sequencing the ends of these DNA fragments and locating their genomic origin using the available genome sequence data, promoter trapping has now been shown to identify real promoters of real genes, exactly as **anticipated**. Developmental **expression patterns** have thereby been linked to gene sequence, allowing further inferences on gene function to be drawn. Some expression patterns generated by promoter trapping include subcellular details. Localization to the surface of particular cells or even particular aspects of the cell surface was found to be consistent with the genes, now associated with these patterns, encoding membrane-spanning proteins. Data on gene expression patterns are easier to generate and characterize than mutant phenotypes and may provide the best means of interpreting the large quantity of sequence data currently being generated in genome projects.

L48 ANSWER 5 OF 6 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 97480734 MEDLINE
DOCUMENT NUMBER: 97480734 PubMed ID: 9339379
TITLE: Differential expression of XAP5, a candidate disease gene.
AUTHOR: Mazzarella R; Pengue G; Yoon J; Jones J; Schlessinger D
CORPORATE SOURCE: Department of Microbiology, Washington University School of Medicine, St. Louis, Missouri 63119, USA.. rich@genetics.wustl.edu
SOURCE: GENOMICS, (1997 Oct 1) 45 (1) 216-9.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AD001530
ENTRY MONTH: 199711
ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 19990129
Entered Medline: 19971120

AB We have isolated a full-length cDNA corresponding to the XAP5 gene in Xq28. An unusual feature of the cDNA is that it contains runs of CCG repeats in the 5' untranslated region, typical of genes that exhibit **anticipation**. It has a striking **pattern** of differential **expression** and is greatly enhanced in various fetal tissues. This predicted protein encodes a unique 339-amino-acid polypeptide that contains a large percentage of highly charged residues and a possible nuclear localization signal. A comparison to genomic sequence shows that XAP-5 comprises 13 exons spanning 6.5 kb. An examination of the human population indicates that the longest CCG run is polymorphic and varies in length from 8 to 12 repeats.

L48 ANSWER 6 OF 6 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 89291517 MEDLINE
DOCUMENT NUMBER: 89291517 PubMed ID: 2472369
TITLE: Distribution of cytokeratin polypeptides in epithelia of the adult human urinary tract.
AUTHOR: Schaafsma H E; Ramaekers F C; van Muijen G N; Ooms E C; Ruiter D J
CORPORATE SOURCE: Department of Pathology, University Hospital Nijmegen, The Netherlands.
SOURCE: HISTOCHEMISTRY, (1989) 91 (2) 151-9.

Journal code: 0411300. ISSN: 0301-5564.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198908
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890803

AB Cytokeratin expression was studied in the epithelia lining the normal human urine conducting system using immunohistochemistry on frozen sections employing a panel of 14 monoclonal antibodies. Eleven of these anticytokeratin antibodies reacted specifically with one of the 19 human cytokeratin polypeptides. Profound differences were found in the cytokeratin expression patterns between the different types of epithelium in the male and female urinary tract. In the areas showing morphological transitions of transitional epithelium to columnar epithelium and of nonkeratinizing squamous epithelium to keratinizing squamous epithelium gradual shifts of cytokeratin **expression patterns** were observed, often **anticipating** the morphological changes. However, also within one type of epithelium, i.e. the transitional epithelium, two different patterns of cytokeratin expression were found. Expression of cytokeratin 7 was homogeneous in the transitional epithelium of renal pelvis and ureter but heterogeneous in the transitional epithelium of the bladder. Furthermore, intraepithelial differences in cytokeratin expression could be shown to be differentiation related. Using a panel of chain-specific monoclonal antibodies to cytokeratins 8 and 18 conformational and/or biochemical changes in the organization of these intermediate filaments were demonstrated upon differentiation in columnar and transitional epithelium.

=> log h

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NEWS 4 Feb 01 DKILIT now produced by FIZ Karlsruhe and has a new update frequency
NEWS 5 Feb 19 Access via Tymnet and SprintNet Eliminated Effective 3/31/02

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 NEWS  6  Mar 08  Gene Names now available in BIOSIS
 NEWS  7  Mar 22  TOXLIT no longer available
 NEWS  8  Mar 22  TRCTHERMO no longer available
 NEWS  9  Mar 28  US Provisional Priorities searched with P in CA/CAplus
                  and USPATFULL
 NEWS 10  Mar 28  LIPINSKI/CALC added for property searching in REGISTRY
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instead.
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 NEWS 16  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and
ZCAPLUS
 NEWS 17  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22  Federal Research in Progress (FEDRIP) now available
 NEWS 19  Jun 03  New e-mail delivery for search results now available
 NEWS 20  Jun 10  MEDLINE Reload
 NEWS 21  Jun 10  PCTFULL has been reloaded
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=> s nadrin or (ras(w)like)
L1 1311 NADRIN OR (RAS(W) LIKE)

=> s l1 and teratocarcinom#
L2 5 L1 AND TERATOCARCINOM#

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 2 DUP REM L2 (3 DUPLICATES REMOVED)

=> d ibib abs tot

L3 ANSWER 1 OF 2 CANCERLIT
ACCESSION NUMBER: 93686556 CANCERLIT
DOCUMENT NUMBER: 93686556
TITLE: Identification and characterization of five novel RAS family genes expressed in a human **teratocarcinoma** cell line.
AUTHOR: Drivas G T
CORPORATE SOURCE: New York Univ.
SOURCE: Diss Abstr Int [B], (1992). Vol. 52, No. 12, pp. 6225. ISSN: 0419-4217.
DOCUMENT TYPE: (THESIS)
FILE SEGMENT: ICDB
LANGUAGE: English
ENTRY MONTH: 199301
AB The RAS gene family codes for a group of low-mol wt (21-25 kD) GTP-binding and hydrolyzing proteins. On the basis of amino acid sequence homology, RAS family genes have been divided into four major groups, termed true RAS, **RAS-like**, RHO and YPT/RAB. Members of the RAS family have been implicated in the regulation of cell growth and division (true RAS), the regulation of vesicle transport (YPT/RAB), and in the maintenance of cell structure (RHO). All RAS family proteins share four highly conserved domains involved in guanine nucleotide binding. We applied two different approaches, both based on the use of oligonucleotides specific for these functional coding domains, to isolate novel human members of each of the major groups of the RAS family. They are TC21 (**RAS-like** subfamily), TC25 and TC10 (RHO subfamily), YL8 (YPT/RAB subfamily) and TC4, a gene whose distinctive characteristics suggest that it defines a new branch of this gene family. Characterization of the isolated cDNAs indicates that these genes are well conserved in mammals, and in some cases, highly homologous to proteins (70-80% identity) recently isolated from fission yeast. Northern analysis of a variety of human and murine cell types reveals markedly different patterns of transcription for these genes; TC4, TC25 and YL8 are generally widely expressed, while TC10 and TC21 are more restricted in their distribution. The cDNAs are capable of encoding proteins in the range of 21-25 kD, and one of these, YL8, has demonstrated GTP-binding ability. Wild-type and mutagenized versions (carrying mutations like those found in

RAS oncoproteins) of TC4, TC21, and TC25 do not show transforming potential in transfected NIH 3T3 fibroblasts. This suggests that their regulatory roles differ from those of true RAS proteins. In the case of TC25, stably transfected 3T3 cell lines overexpressing this cDNA product display an altered cellular morphology, a finding consistent with the proposed role of RHO group proteins. (Full text available from University Microfilms International, Ann Arbor, MI, as Order No. AAD92-13224)

L3 ANSWER 2 OF 2 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 90205863 MEDLINE
DOCUMENT NUMBER: 90205863 PubMed ID: 2108320
TITLE: Characterization of four novel **ras-like** genes expressed in a human **teratocarcinoma** cell line.
AUTHOR: Drivas G T; Shih A; Coutavas E; Rush M G; D'Eustachio P
CORPORATE SOURCE: Department of Biochemistry, New York University School of Medicine, New York 10016.
CONTRACT NUMBER: ES03847 (NIEHS)
GM07827 (NIGMS)
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, (1990 Apr) 10 (4) 1793-8.

Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M31467; GENBANK-M31468; GENBANK-M31469; GENBANK-M31470
ENTRY MONTH: 199005
ENTRY DATE: Entered STN: 19900601
Last Updated on STN: 20000303
Entered Medline: 19900502

AB A mixed-oligonucleotide probe was used to identify four **ras-like** coding sequences in a human **teratocarcinoma** cDNA library. Two of these sequences resembled the rho genes, one was closely related to H-, K-, and N-ras, and one shared only the four sequence domains that define the ras gene superfamily. Homologs of the four genes were found in genomic DNA from a variety of mammals and from chicken. The genes were transcriptionally active in a range of human cell types.

```
=> s drivas?/au
L4          204 DRIVAS?/AU

=> s l4 and ras
L5           35 L4 AND RAS

=> s l5 and py<2002
   2 FILES SEARCHED...
   4 FILES SEARCHED...
L6           35 L5 AND PY<2002

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7           11 DUP REM L6 (24 DUPLICATES REMOVED)

=> d ibib abs tot

L7   ANSWER 1 OF 11     MEDLINE                          DUPLICATE 1
ACCESSION NUMBER:   97003732     MEDLINE
DOCUMENT NUMBER:    97003732   PubMed ID: 8851043
```

TITLE: The small nuclear GTPase Ran: how much does it run?.
AUTHOR: Rush M G; **Drivas G**; D'Eustachio P
CORPORATE SOURCE: Department of Biochemistry, New York University Medical Center, NY 10016, USA.
SOURCE: BIOESSAYS, **(1996 Feb)** 18 (2) 103-12. Ref: 70
Journal code: 8510851. ISSN: 0265-9247.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 20000303
Entered Medline: 19961206

AB Ran is one of the most abundant and best conserved of the small GTP binding and hydrolyzing proteins of eukaryotes. It is located predominantly in cell nuclei. Ran is a member of the **Ras** family of GTPases, which includes the **Ras** and **Ras**-like proteins that regulate cell growth and division, the Rho and Rac proteins that regulate cytoskeletal organization and the Rab proteins that regulate vesicular sorting. Ran differs most obviously from other members of the **Ras** family in both its nuclear localization, and its lack of sites required for post-translational lipid modification. Ran is, however, similar to other **Ras** family members in requiring a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. In this review, the multiple cellular functions of Ran are evaluated with respect to its known biochemistry and molecular interactions.

L7 ANSWER 2 OF 11 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 94254867 MEDLINE
DOCUMENT NUMBER: 94254867 PubMed ID: 8196649
TITLE: Aberrant function of the **Ras**-related protein TC21/R-Ras2 triggers malignant transformation.
AUTHOR: Graham S M; Cox A D; **Drivas G**; Rush M G; D'Eustachio P; Der C J
CORPORATE SOURCE: University of North Carolina at Chapel Hill 27599.
CONTRACT NUMBER: CA42978 (NCI)
CA52072 (NCI)
CA55008 (NCI)
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, **(1994 Jun)** 14 (6) 4108-15.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199406
ENTRY DATE: Entered STN: 19940707
Last Updated on STN: 19980206
Entered Medline: 19940624

AB Although the human **Ras** proteins are members of a large superfamily of **Ras**-related proteins, to date, only the proteins encoded by the three mammalian **ras** genes have been found to possess oncogenic potential. Among the known **Ras**-related proteins, TC21/R-Ras2 exhibits the most significant amino acid identity (55%) to **Ras** proteins. We have generated mutant forms of TC21 that possess amino acid substitutions analogous to those that activate

Ras oncogenic potential [designated TC21(22V) and TC21(71L)] and compared the biological properties of TC21 with those of **Ras** proteins in NIH 3T3 and Rat-1 transformation assays. Whereas wild-type TC21 did not show any transforming potential in vitro, both TC21(22V) and TC21(71L) displayed surprisingly potent transforming activities that were comparable to the strong transforming activity of oncogenic **Ras** proteins. Like **Ras**-transformed cells, NIH 3T3 cells expressing mutant TC21 proteins formed foci of morphologically transformed cells in monolayer cultures, proliferated in low serum, formed colonies in soft agar, and developed progressive tumors in nude mice. Thus, TC21 is the first **Ras**-related protein to exhibit potent transforming activity equivalent to that of **Ras**. Furthermore, mutant TC21 proteins also stimulated constitutive activation of mitogen-activated protein kinases as well as transcriptional activation from **Ras** -responsive promoter elements (Ets/AP-1 and NF-kappa B). We conclude that aberrant TC21 function may trigger cellular transformation via a signal transduction pathway similar to that of oncogenic **Ras** and suggest that deregulated TC21 activity may contribute significantly to human oncogenesis.

L7 ANSWER 3 OF 11 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 95152168 MEDLINE
DOCUMENT NUMBER: 95152168 PubMed ID: 7849398
TITLE: Tissue-specific expression of Ran isoforms in the mouse.
AUTHOR: Coutavas E E; Hsieh C M; Ren M; **Drivas G T**; Rush M G; D'Eustachio P D
CORPORATE SOURCE: Department of Biochemistry, New York University Medical Center, New York 10016.
CONTRACT NUMBER: GM07827 (NIGMS)
SOURCE: MAMMALIAN GENOME, **(1994 Oct)** 5 (10) 623-8.
Journal code: 9100916. ISSN: 0938-8990.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L32751; GENBANK-L32752
ENTRY MONTH: 199503
ENTRY DATE: Entered STN: 19950322
Last Updated on STN: 20000303
Entered Medline: 19950316

AB Ran genes encode a family of well-conserve small nuclear GTPases (**Ras**-related nuclear proteins), whose function is implicated in both normal cell cycle progression and the transport of RNA and proteins between the nucleus and the cytoplasm. Previous studies of Ran proteins have utilized cell-free systems, yeasts, and cultured mammalian cells. We have now characterized patterns of Ran gene expression in the mouse. Serum starvation suppressed Ran gene transcription in mouse 3T3 cells. Ran mRNA reappeared in cells within 3 h after refeeding. A single Ran mRNA species was detected at low levels in most somatic tissues of the adult mouse. In testis, this Ran mRNA was abundant, as were other larger transcripts. Analysis of testis-derived Ran cDNA clones revealed the presence of two transcripts, one specifying an amino acid sequence identical to that of human Ran/TC4 and one specifying an amino acid sequence 94% identical. Northern blotting and reverse transcriptase-PCR assays with oligonucleotide probes and primers specific for each transcript demonstrated that the isoform identical to Ran/TC4 was expressed in both somatic tissues and testis, while the variant form was transcribed only in testis. The existence of tissue-specific Ran isoforms may help to rationalize the diverse roles suggested for Ran by previous biochemical

studies.

L7 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:74241 CAPLUS
DOCUMENT NUMBER: 122:47573
TITLE: Identification of novel **ras** family genes in a human teratocarcinoma cell line by oligonucleotide screening
AUTHOR(S): **Drivas, George T.**; Rush, Mark G.; D'Eustachio, Peter
CORPORATE SOURCE: Sch. Med., New York Univ., New York, NY, USA
SOURCE: ras Superfamily GTPases (**1993**), 329-47. Editor(s): Lacal, Juan Carlos; McCormick, Frank. CRC: Boca Raton, Fla.
CODEN: 60MXA3
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review with 53 refs.

L7 ANSWER 5 OF 11 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 93132064 MEDLINE
DOCUMENT NUMBER: 93132064 PubMed ID: 8421051
TITLE: Ran/TC4: a small nuclear GTP-binding protein that regulates DNA synthesis.
AUTHOR: Ren M; **Drivas G**; D'Eustachio P; Rush M G
CORPORATE SOURCE: Department of Cell Biology, New York University Medical Center, NY 10016.
CONTRACT NUMBER: GM07827 (NIGMS)
RR083990 (NCRR)
SOURCE: JOURNAL OF CELL BIOLOGY, **(1993 Jan)** 120 (2) 313-23.
Journal code: 0375356. ISSN: 0021-9525.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M31469
ENTRY MONTH: 199302
ENTRY DATE: Entered STN: 19930226
Last Updated on STN: 20000303
Entered Medline: 19930217
AB Ran/TC4, first identified as a well-conserved gene distantly related to H-**RAS**, encodes a protein which has recently been shown in yeast and mammalian systems to interact with RCC1, a protein whose function is required for the normal coupling of the completion of DNA synthesis and the initiation of mitosis. Here, we present data indicating that the nuclear localization of Ran/TC4 requires the presence of RCC1. Transient expression of a Ran/TC4 protein with mutations expected to perturb GTP hydrolysis disrupts host cell DNA synthesis. These results suggest that Ran/TC4 and RCC1 are components of a GTPase switch that monitors the progress of DNA synthesis and couples the completion of DNA synthesis to the onset of mitosis.

L7 ANSWER 6 OF 11 CANCERLIT
ACCESSION NUMBER: 93686556 CANCERLIT
DOCUMENT NUMBER: 93686556
TITLE: Identification and characterization of five novel **RAS** family genes expressed in a human

teratocarcinoma cell line.
AUTHOR: **Drivas G T**
CORPORATE SOURCE: New York Univ.
SOURCE: Diss Abstr Int [B], **(1992)**. Vol. 52, No. 12, pp. 6225.
ISSN: 0419-4217.
DOCUMENT TYPE: (THESIS)
FILE SEGMENT: ICDB
LANGUAGE: English
ENTRY MONTH: 199301
AB The **RAS** gene family codes for a group of low-mol wt (21-25 kD) GTP-binding and hydrolyzing proteins. On the basis of amino acid sequence homology, **RAS** family genes have been divided into four major groups, termed true **RAS**, **RAS**-like, RHO and YPT/RAB. Members of the **RAS** family have been implicated in the regulation of cell growth and division (true **RAS**), the regulation of vesicle transport (YPT/RAB), and in the maintenance of cell structure (RHO). All **RAS** family proteins share four highly conserved domains involved in guanine nucleotide binding. We applied two different approaches, both based on the use of oligonucleotides specific for these functional coding domains, to isolate novel human members of each of the major groups of the **RAS** family. They are TC21 (**RAS** -like subfamily), TC25 and TC10 (RHO subfamily), YL8 (YPT/RAB subfamily) and TC4, a gene whose distinctive characteristics suggest that it defines a new branch of this gene family. Characterization of the isolated cDNAs indicates that these genes are well conserved in mammals, and in some cases, highly homologous to proteins (70-80% identity) recently isolated from fission yeast. Northern analysis of a variety of human and murine cell types reveals markedly different patterns of transcription for these genes; TC4, TC25 and YL8 are generally widely expressed, while TC10 and TC21 are more restricted in their distribution. The cDNAs are capable of encoding proteins in the range of 21-25 kD, and one of these, YL8, has demonstrated GTP-binding ability. Wild-type and mutagenized versions (carrying mutations like those found in **RAS** oncoproteins) of TC4, TC21, and TC25 do not show transforming potential in transfected NIH 3T3 fibroblasts. This suggests that their regulatory roles differ from those of true **RAS** proteins. In the case of TC25, stably transfected 3T3 cell lines overexpressing this cDNA product display an altered cellular morphology, a finding consistent with the proposed role of RHO group proteins. (Full text available from University Microfilms International, Ann Arbor, MI, as Order No. AAD92-13224)

L7 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:118003 CAPLUS
DOCUMENT NUMBER: 118:118003
TITLE: Identification and characterization of five novel **RAS** family genes expressed in a human teratocarcinoma cell line
AUTHOR(S): **Drivas, George Theodore**
CORPORATE SOURCE: New York Univ., New York, NY, USA
SOURCE: **(1991)** 116 pp. Avail.: Univ. Microfilms Int., Order No. DA9213224
From: Diss. Abstr. Int. B 1992, 52(12, Pt. 1), 6225
DOCUMENT TYPE: Dissertation
LANGUAGE: English
AB Unavailable

L7 ANSWER 8 OF 11 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 91248193 MEDLINE
DOCUMENT NUMBER: 91248193 PubMed ID: 2039498
TITLE: Evolutionary grouping of the **RAS**-protein family.

AUTHOR: **Drivas G T**; Palmieri S; D'Eustachio P; Rush M G
CORPORATE SOURCE: Department of Biochemistry, New York University School of Medicine, New York 10016.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, **(1991 May 15)** 176 (3) 1130-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199107
ENTRY DATE: Entered STN: 19910719
Last Updated on STN: 20000303
Entered Medline: 19910703

AB Over 50 proteins related to the mammalian H-, K-, and N-**RAS** GTP binding and hydrolyzing proteins are known. These relatively low molecular weight proteins are usually grouped into four subfamilies, termed true **RAS**, **RAS**-like, RHO, and RAB/YPT, based on the presence of shared amino acid sequence motifs in addition to those involved in guanine nucleotide binding. Here, we apply parsimony analysis to the overall amino acid sequences of these proteins to infer possible phylogenetic relationships among them.

L7 ANSWER 9 OF 11 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 92190844 MEDLINE
DOCUMENT NUMBER: 92190844 PubMed ID: 1686838
TITLE: **Ras**-like genes and gene families in the mouse.
AUTHOR: **Drivas G**; Massey R; Chang H Y; Rush M G; D'Eustachio P
CORPORATE SOURCE: Department of Biochemistry, New York University Medical Center, New York 10016.
SOURCE: MAMMALIAN GENOME, **(1991)** 1 (2) 112-7.
Journal code: 9100916. ISSN: 0938-8990.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199204
ENTRY DATE: Entered STN: 19920509
Last Updated on STN: 20000303
Entered Medline: 19920420

AB Four human **RAS**-like cDNAs and a mouse genomic DNA fragment were used to define novel mouse **Ras**-like genes and gene families. Inheritance of DNA restriction fragment length variants associated with these genes in recombinant inbred and backcross mice allowed definition of 12 genetic loci, nine of which were mapped, to chromosomes (Chr) 2, 4, 7, 8, 9, and 17. Two possible clusters of **Ras**-like and/or G protein genes were identified, on Chrs 9 and 17.

L7 ANSWER 10 OF 11 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 91125876 MEDLINE
DOCUMENT NUMBER: 91125876 PubMed ID: 1704119
TITLE: Identification and characterization of a human homolog of the Schizosaccharomyces pombe **ras**-like gene YPT-3.
AUTHOR: **Drivas G T**; Shih A; Coutavas E E; D'Eustachio P; Rush M G
CORPORATE SOURCE: Department of Biochemistry, New York University School of Medicine, New York 10016.

CONTRACT NUMBER: GM07827 (NIGMS)
SOURCE: ONCOGENE, **(1991 Jan)** 6 (1) 3-9.
Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-S77853; GENBANK-S77855; GENBANK-S77857;
GENBANK-S77862; GENBANK-S77864; GENBANK-S77866;
GENBANK-S77870; GENBANK-S77874; GENBANK-S77877;
GENBANK-X53143
ENTRY MONTH: 199103
ENTRY DATE: Entered STN: 19910405
Last Updated on STN: 19960129
Entered Medline: 19910308

AB The Polymerase Chain Reaction was used to amplify **ras** and **ras**-like sequences from two human cDNA libraries. Members corresponding to each of the three major **ras**-subfamilies (**ras**, rho, and rab/YPT) were identified. The one homologous to rab/YPT, referred to here as YL8, appears to be the human homolog of the recently reported Schizosaccharomyces pombe YPT3 gene. The YL8 gene could encode a guanine nucleotide binding protein of 216 amino acids with about 70% amino acid sequence identity to S. pombe YPT3, and is transcriptionally active in a variety of human cell lines.

L7 ANSWER 11 OF 11 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 90205863 MEDLINE
DOCUMENT NUMBER: 90205863 PubMed ID: 2108320
TITLE: Characterization of four novel **ras**-like genes expressed in a human teratocarcinoma cell line.
AUTHOR: **Drivas G T**; Shih A; Coutavas E; Rush M G; D'Eustachio P
CORPORATE SOURCE: Department of Biochemistry, New York University School of Medicine, New York 10016.
CONTRACT NUMBER: ES03847 (NIEHS)
GM07827 (NIGMS)
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, **(1990 Apr)** 10 (4) 1793-8.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M31467; GENBANK-M31468; GENBANK-M31469;
GENBANK-M31470
ENTRY MONTH: 199005
ENTRY DATE: Entered STN: 19900601
Last Updated on STN: 20000303
Entered Medline: 19900502

AB A mixed-oligonucleotide probe was used to identify four **ras**-like coding sequences in a human teratocarcinoma cDNA library. Two of these sequences resembled the rho genes, one was closely related to H-, K-, and N-**ras**, and one shared only the four sequence domains that define the **ras** gene superfamily. Homologs of the four genes were found in genomic DNA from a variety of mammals and from chicken. The genes were transcriptionally active in a range of human cell types.

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